

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2006, 08:14:53 ; Search time 149 Seconds  
(without alignments)  
7509.551 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 597

Sequence: 1 gcgctgctgcagacgcgc.....agccatttcgcaccaaagcc 598

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/prodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/prodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.2	16.3	381	3	Sequence 5776, Ap
2	97.2	16.3	72704	3	Sequence 1273, Ap
C 3	46.4	7.8	4403765	3	Sequence 2, Appli
C 4	46.4	7.8	4411529	3	Sequence 1, Appli
5	45.2	7.6	1143	3	Sequence 8600, Ap
6	45.2	7.6	6821	3	Sequence 907, App
7	43.4	7.3	603	3	Sequence 14, Appl
8	43.4	7.3	603	3	Sequence 1, Appli
9	42.8	7.2	585	3	Sequence 5853, Ap
10	42.8	7.2	19019	3	Sequence 3555, Ap
11	42.6	7.1	3128	3	Sequence 1171, Ap
12	42.6	7.1	26896	3	Sequence 1, Appli
13	42.2	7.1	759	3	Sequence 16800, A
14	42	7.0	1058	3	Sequence 11092, A
15	41.6	7.0	969	3	Sequence 11092, A
16	41.6	7.0	1280	3	Sequence 8164, Ap
17	41.6	7.0	1280	3	Sequence 4, Appli
18	41.6	7.0	1280	3	Sequence 4, Appli
19	41.6	7.0	1280	3	Sequence 4, Appli
20	41.6	7.0	1491	3	Sequence 9, Appli
21	41.6	7.0	1524	3	Sequence 9, Appli
22	41.6	7.0	1817	3	Sequence 3, Appli
23	41.6	7.0	2887	3	Sequence 45, Appli
					Sequence 1, Appli

24	41.6	7.0	3083	2	US-08-480-994-36	Sequence 36, Appl
25	41.6	7.0	3083	2	US-08-616-844-36	Sequence 36, Appl
26	41.6	7.0	3083	2	US-08-599-654-36	Sequence 36, Appl
27	41.6	7.0	3083	2	US-08-485-573-36	Sequence 36, Appl
28	41.6	7.0	3083	3	US-08-944-868A-36	Sequence 36, Appl
29	41.6	7.0	3083	3	US-08-944-423A-36	Sequence 36, Appl
30	41.6	7.0	3083	3	US-08-925-743-36	Sequence 36, Appl
31	41.6	7.0	3083	3	US-08-944-496-36	Sequence 36, Appl
32	41.6	7.0	3083	3	US-08-925-767-36	Sequence 36, Appl
33	41.6	7.0	3084	3	US-08-826-246-11	Sequence 11, Appl
34	41.6	7.0	3084	3	US-08-944-495-11	Sequence 11, Appl
35	41.6	7.0	3084	3	US-09-126-640-6	Sequence 6, Appli
36	41.6	7.0	3084	3	US-08-925-588-11	Sequence 6, Appli
37	41.6	7.0	3084	3	US-09-288-292A-6	Sequence 11, Appl
38	41.6	7.0	3084	3	US-09-372-044-11	Sequence 11, Appl
39	41.6	7.0	3084	3	US-08-825-486-11	Sequence 11, Appl
40	41.6	7.0	3084	3	US-08-826-248-11	Sequence 11, Appl
41	41.6	7.0	5663	3	US-09-902-540-839	Sequence 839, App
42	41.2	6.9	3066	3	US-09-902-540-9635	Sequence 9635, Ap
43	41.2	6.9	15782	3	US-09-902-540-1094	Sequence 1094, Ap
44	41	6.9	1440	3	US-09-902-540-9640	Sequence 9640, Ap
45	41	6.9	15782	3	US-09-902-540-1094	Sequence 1094, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-902-540-5776  
; Sequence 5776, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5776  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5776

Query Match 16.3%; Score 97.2; DB 3; Length 381;  
Best Local Similarity 56.9%; Pred. No. 1e-15;  
Matches 199; Conservative 0; Mismatches 148; Indels 3; Gaps 1;  
QY 61 AAGAGCTGTTTGTAGCTGGCGCGCCAGAGGCATGAAGCTGGCGTTGACACTTC 120  
DB 19 AAGATGTTCTAGCAGCTGGCGCGAGAGCGCGCATGGCGCGGTGGAGGTCTTC 78  
QY 121 TACCATAAGGTGCTGGCTGACCCCGAGCTGCTCCCTTCTTCAGTTCCTTGGGAGCATGCAA 180  
DB 79 TACCGAAGGTGCTGGCGCGAGCATCATCAGCCACTTCTTCGAGCATGGAGTGGAG 138  
QY 181 GAGCAGAAAGTGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATAC 240  
DB 139 GCCCAGGCGCGAGCAGCAGAGCGTTCCTGACGATGGTGGCGGTGGCGGTGGCGGTTCAC 198  
QY 241 AAGGCGCAGACATGTACGACGACACGCCCATCTGTGTCAAGGGCCACGGCTTGGACCAAC 300  
DB 199 TCGGCAAGGACATCGCGCGCGCCACGCGCTCTGTGTAAG---CGTGGGTGAACGAC 255  
QY 301 CGCCACTTTGACAAGATCAACAGTACCTTGGAGAGCGCTGCAAGAGATGGCGTCAAG 360  
DB 256 TCGCACTTCGACGCGGTGGCGGGCCACCTGAAGGCGACGCTGGAGGAGCTGGGCGTGGCC 315

Best Local Similarity 51.9%; Pred. No. 0.23;  
Matches 95; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 53 GCGGGCGGAGAGCTGTTGATGACCTGGCGGCGGCGAGAGCATGAAGCTGGCGGTG 112  
Db 500 GCGAGCGGAAGTGGTGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGTA 559  
QY 113 ACACCTTCTACGATAAGGTGCTGGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGG 172  
Db 560 CGCTCGTGGGAGCGGAGCTGGCTACTTCGACTTCAACACAGCTTTCGCGCCCTGC 619  
QY 173 ACATCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTGGCGGAGCAG 232  
Db 620 ATCGACACTGGAGAAGCTGGAGCAGGACCGCGGCGTGGCTTCGCCCATGCGATCGAGG 679  
QY 233 ACC 235  
Db 680 ATC 682

RESULT 14  
US-09-452-239-11  
; Sequence 11, Application US/09452239  
; Patent No. 6465229  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni J.  
; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase  
; FILE REFERENCE: B1284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; PRIORITY FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 11  
; LENGTH: 1058  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-452-239-11

Query Match 7.0%; Score 42; DB 3; Length 1058;  
Best Local Similarity 52.9%; Pred. No. 0.28;  
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 162 CGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTT 221  
Db 619 CAACCTCACTCACTACACAGAGCGGCTGATGAAGCTGTCAGGTGCGGCGGCTTCGTGG 678  
QY 222 TGGCGGAGCAGACCAATACAAAGGCGGCGGAGCATGTACGACACAGCCCATCTGGTCAA 281  
Db 679 CTACGACAAACAGCTCTGGAACGGCTCGTGTCTCCCGCGGAGCGCCCATGCGGCAA 738  
QY 282 GGGCGAGCGCTGGACACCGCCACTTTGCAAGATCAAGCAGTACCTTG 331  
Db 739 GTACATCGCTACTACCGCGACTTCGTGCTCGAGCTCAACAAAGGCCCTCG 788

RESULT 15  
US-09-902-540-8164  
; Sequence 8164, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIORITY FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8164  
; LENGTH: 969  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8164  
Query Match 7.0%; Score 41.6; DB 3; Length 969;  
Best Local Similarity 43.9%; Pred. No. 0.35;  
Matches 176; Conservative 0; Mismatches 225; Indels 0; Gaps 0;  
QY 21 CACCAGCACACAGAGACGCGGAAGCGGATGCGGCGGCGCAAGAAGCTGTTTGTGATGACCT 80  
Db 402 CACCACCTGAGCAGACGCTGGACCCGCGACAGGTGCTGGAGTTGCTGGACGACTACTT 461  
QY 81 GGGCGGCGCAGAAGGCATGAAGCTGGCGGTGACACCTTCTTACGATAAGGTGCTGGCTGA 140  
Db 462 CGGSCACATGSCCACCACATCGTCATGGCGCGCCACGGCATCGTGAACAAGTTCTCTGGGCGA 521  
QY 141 CCGGAGCTGTCGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGT 200  
Db 522 CGGATGCTCGCGTGTGGGCGGTTCCGGATGCGCGGAGAACCCACGCGAGCTGGCCAT 581  
QY 201 CAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGCGGCGGAGCATGTACGA 260  
Db 582 GCGGCGGCGCTCGACATGCGCGCAAGCTGGAGGACATCAACGCCCGCGGCGTGCAGCG 641  
QY 261 CGCACACGCGCCATCTGTCGAAGGCGCACCGCTGGACCGCCACTTTGACAAAGATCAA 320  
Db 642 AGTCTGCGCGCGCTGGCATCGGCATCGGCTGCGACACCGGCATGCTGGCGGCGGCGAT 701  
QY 321 GCAGTACCTTTGGAGAGACGCTGCAAGAGATGGGCGTCAAGCAGGATGTGATCCAGCAGCG 380  
Db 702 GCTCGGCGGCGGAGCAGCAGTACACCGTCAATCGGTGACGCGGTGAACCTGGCGTC 761  
QY 381 CGCGGAGTGTGGAGTCCACCGCGCAGCAATTTGACTTNC 421  
Db 762 TCGGTGGAGGCGCTCACCAGTCCACCGCGTGGACATCC 802

Search completed: August 12, 2006, 08:19:31  
Job time : 156 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2006, 08:17:05 ; Search time 1175 Seconds  
(without alignments)  
6253.622 Million cell updates/sec

Title: US-09-920-953-2  
Perfect score: 597  
Sequence: 1 ggcgtccgcagacggc.....agccatttcgaccagcc 598

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES.

Result No.	Score	Query Match	ID	Description
1	74.4	12.5	372	US-10-282-122A-25335 Sequence 25335, A
2	50.8	8.5	1694969	US-10-506-454-1690 Sequence 1690, Ap
3	50	8.4	2466	US-10-156-761-5788 Sequence 5788, Ap
4	50	8.4	9025608	US-10-156-761-1 Sequence 1, Appli
5	47.6	8.0	2256646	US-10-470-565-1 Sequence 1, Appli
6	47.4	7.9	548	US-10-437-963-94550 Sequence 94550, A
7	46.6	7.8	1389	US-10-411-910A-255 Sequence 255, App
8	46.6	7.8	1389	US-10-411-910A-257 Sequence 257, App
9	46.2	7.7	1209	US-10-369-493-32038 Sequence 32038, A
10	46.2	7.7	1509	US-10-411-910A-264 Sequence 264, App
11	45.8	7.7	2209	US-10-437-963-69229 Sequence 69229, A
12	45.2	7.6	2238	US-10-437-963-97363 Sequence 97363, A
13	45.2	7.6	3743	US-10-502-351-1 Sequence 1, Appli
14	44.4	7.4	1445	US-10-437-963-35783 Sequence 35783, A
15	44.2	7.4	1000	US-10-389-566-49 Sequence 49, Appli
16	44.2	7.4	1377	US-10-369-493-39791 Sequence 39791, A
17	44.2	7.4	1395	US-10-369-493-39403 Sequence 39403, A

Sequence 39036, A  
Sequence 235, App  
Sequence 7459, Ap  
Sequence 72, Appl  
Sequence 60, Appl  
Sequence 32926, A  
Sequence 108376, A  
Sequence 11546, A  
Sequence 4715, Ap  
Sequence 23705, A  
Sequence 30, Appl  
Sequence 18, Appl  
Sequence 95877, A  
Sequence 4532, Ap  
Sequence 419, App  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 2429, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 5556, Ap  
Sequence 215, App  
Sequence 6685, Ap  
Sequence 4170, Ap  
Sequence 5, Appli  
Sequence 3, Appli  
Sequence 11, Appl

## ALIGNMENTS

## RESULT 1

US-10-282-122A-25335  
Sequence 25335, Application US/10282122A  
Publication No. US20040029129A1

## GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25335  
; LENGTH: 372  
; TYPE: DNA  
; ORGANISM: Legionella pneumophila  
US-10-282-122A-25335

Query Match 12.5%; Score 74.4; DB 8; Length 372;  
Best Local Similarity 54.0%; Pred. No. 1e-12;  
Matches 175; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

QY 68 TGTTTATGACCTGGCGCGCGAAGGATGAAGCTGGCGGTGACATCTTCTACGATA 127  
DB 14 TGTGTTGAGCGATTAGCGCGCAAAATGCCGTCAACACAGCTGTGGATATTTCTACCGCA 73

QY 128 AGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGACAGA 187  
DB 74 AATGCTCATGATGACAGAGTGAATATTTTTCATGACGTGGATATGGAGCAACAAA 133

QY 188 AGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATCAAGGGCC 247  
DB 134 TCCTTAAGCAAAAGATTTTAAACCATGTTGTTGGCGGACCAATCAATCACTGGAA 193

QY 248 GAAGCATGTACGACGACACACGCCCATCTGTTCAAGGGCCACGCGCTGGACCGCCACT 307  
DB 194 AAGATATGCGGGAAGACATCAGCATCTACT--TGCCAGAGGCTTAAATGACTCACATG 250

QY 308 TTGACAGATCAAGCAGTACCTTGGAGACACGCTGCAAGAGATGGCGTCAAGCAGGATG 367  
DB 251 TGGATATTGTAATCGAGCATTTAGGGGAAACCCCTTAAGGAATTTGGCGCAATGAAGAGG 310

QY 368 TGATCAGCAGCGCGCGGAGTGG 391  
DB 311 ACATTCAGAAAGTAGTCGAATCG 334

RESULT 2  
US-10-506-454-1690  
; Sequence 1690, Application US/10506454  
; Publication No. US20060068386A1  
; GENERAL INFORMATION:  
; APPLICANT: Slesarev, Alexi I  
; APPLICANT: Mezheva, Katja V  
; APPLICANT: Polushin, Nikolai N  
; APPLICANT: Shcherbinina, Olga V  
; APPLICANT: Shakhova, Vera V  
; APPLICANT: Malykh, Andrei G  
; APPLICANT: Kozyavkin, Sergei A  
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile  
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens  
; FILE REFERENCE: FID001  
; CURRENT APPLICATION NUMBER: US/10/506,454  
; CURRENT FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: PCT/US03/06664  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/361,742  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 1722  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1690  
; LENGTH: 1694969  
; TYPE: DNA  
; ORGANISM: Methanopyrus kandleri  
US-10-506-454-1690

Query Match 8.5%; Score 50.8; DB 12; Length 1694969;  
Best Local Similarity 47.5%; Pred. No. 0.0004;  
Matches 151; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 53 GCGGCGCAAGAAGCTGTTTATGATACCTGGCGGCGCAGAAGCATGAAGCTGGCGGTTG 112  
DB 966058 GCATGGACAAGATGCTGTCGACGAGATGGGCGAGCTGCTGTGTGACCAACGACGGTGTAA 966117

QY 113 ACACCTTTTACGATAAGGTGCTGGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGG 172  
DB 966118 CCATCTTGAGGAGATGACATCGAGACCCCGCGCTGAAGATGCTGTTGAGGATCGCCA 966177

QY 173 ACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAG 232  
DB 966178. AGACCGCAGGAGCAGGCTGGTACGACACGCGCTGCTGCTCGCGGTGAGC 966237

QY 233 ACCAATCAAGGCGCGAAGCATGTACGACGACACGCCCATCTGTTAAAGGCGCACGGCC 292  
DB 966238 TGCTGCACAAGGCGCGAGGATCTACTGTCAGCAGGACATCCACCCGCTGATCGCACGG 966297

QY 293 TGGACCCGCGCACCTTTCACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATCG 352  
DB 966298 GTTACCGAATGGCCGTCGAAAAGGCCGAGGATCTCTTGGAGAGATCGCCGAAGAGATCG 966357

QY 353 GCGTCAAGCAGGATGTGA 370  
DB 966358 ACCCGATGACGAGGAGA 966375

RESULT 3  
US-10-156-761-5788  
; Sequence 5788, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 5788  
; LENGTH: 2466  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2466)  
US-10-156-761-5788

Query Match 8.4%; Score 50; DB 7; Length 2466;  
Best Local Similarity 47.1%; Pred. No. 9.7e-05;  
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 115 ACCTTTACGATAAGGTGCTGGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGAC 174  
DB 421 ACCTCCCACTGCTGCTGCCGAGGACCCGCGCTGCTGGCGGCGACGCGCGCTGGTC 480

QY 175 ATGCAAGAGCAGAAGATGAAGCAGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAG 234  
DB 481 CTGGTCGACGAGGATTTCTCCACCGCAACACGGTTCCTCAACACCATCCGCGCTGCAC 540

QY 235 CAATACAGGCGCGAAGCATGTACGACGACACGCCCATCTGGTCAAGGCGCACGGCCTG 294  
DB 541 GAGCGCTATCCGCGCGCGGTACGTGCTGCTGCCCTCGTGGACATCGGCTCCCGGCC 600

QY 295 GACCACCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCC 354  
|||||

Db 601 GACCTCGGCGCTGACGAGTTCCGCGCGAGATCGGTGCCCGGTGACCTGATCAGC 660  
QY 355 GTCAACGACGATGTGATCAGACAGCGCGCGGAGTGGTGCAGTCCACCGCGACGAATTT 414  
Db 661 GCGCGCTCGGCGACGCTGAAGTGTCCCGAGGGCGTCTGGAGAAGGGCGAGGCTGGTC 720  
QY 415 GACTTNCACCAACACTGCGCACC 437  
Db 721 GCCCGCACGAGAGGCCGTACC 743

## RESULT 4

US-10-156-761-1  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156, 761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1  
; LENGTH: 9025608  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4187715)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 8.4%; Score 50; DB 7; Length 9025608;  
Best Local Similarity 47.1%; Pred. No. 0.0012;  
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;  
QY 115 ACCTTCTACGATAAGTGTGCTGACCCGAGCTGCTGCCCTTCTTTCAGTCCCTGGAC 174  
Db 7015347 ACCTCCACCTGCTGCTGCCGAGACCCGCGCTGCTGGCGGGCGACGGCCCGTGGTC 7015406  
QY 175 ATGCAAGACGAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTGGCGGACGAC 234  
Db 7015407 TGGTTCGACGACGAGTTCTCCACCGCAACCGGTCTCAACACCATCCGCGACCTGCAC 7015466  
QY 235 CAATACAGGGCCGGAAGCATGTACACGACACACGCCCATCTGTCAGGGCCACGGCTG 294  
Db 7015467 GAGCGCTATCCGCGCGCGGCGGTACGTCGTCGCGCTCTGGAGATCGCTCCCGGCC 7015526  
QY 295 GACCAACCGCCACTTTGACAAGATCAAGCAGTAGTACCTTGGAGACGCTGCAAGAGATGGC 354  
Db 7015527 GACCTCGGGCGCTGAGAGTTCGCGCGAGATCGGTGCCCGGTGACCTGATCAGG 7015586  
QY 355 GTCAAGCAGGATGTGATCAGACACCGCGCGAGTGGTGGAGTCCACCGCGACGAATTT 414  
Db 7015587 GCGCGCTCGGGACGCTGAAGTGTCCCGAGGCGTGTGGAGAAGGGCGAGGCTGGTC 7015646  
QY 415 GACTTNCACCAACACTGCGCACC 437  
Db 7015647 GCCCGCACGAGAGGCCGTACC 7015669

## RESULT 5

US-10-470-565-1/c

; Sequence 1, Application US/10470565  
; Publication No. US20040126870A1  
; GENERAL INFORMATION:  
; APPLICANT: Societe des Produits Nestle S.A.  
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium  
; FILE REFERENCE: 80290/WO  
; CURRENT APPLICATION NUMBER: US/10/470, 565  
; CURRENT FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: EP 01102050.0  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2256646  
; TYPE: DNA  
; ORGANISM: Bifidobacterium longum  
US-10-470-565-1  
Query Match 8.0%; Score 47.6; DB 8; Length 2256646;  
Best Local Similarity 44.6%; Pred. No. 0.0045;  
Matches 185; Conservative 0; Mismatches 230; Indels 0; Gaps 0;  
QY 15 CGCGGCCACACGACACACGAGAGCGGCGGAAGCGGGATCGCGGCGCAAGAAAGCTGTTTCA 74  
Db 1432814 CGTCTCTACTTTCACGCGAGCATGGGTATGCACTGGCCACAGCAACCCCAAGACGT 1432755  
QY 75 TGACCTGGCGCGCAGAAAGCATGAAGCTGGCGGTGACACCTTCTACGATAAGGTGCT 134  
Db 1432754 CGATGAGAAACGACCTGTGCGGTCTGAAGCTTGGCGTGCAGACCGGACCGTGCAGGAAGA 1432695  
QY 135 GGCTGACCCGAGCTGTGCGCTTCTTCGAGTCCCTGACATGCAAGAGCAGCAAGATGAA 194  
Db 1432694 GGCCATCAACAAGACCCGCCAAGCAGTGCAGGCGGACCGCAAGAAAGACATCACCATCCA 1432635  
QY 195 CGAGGTCAAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGGCCGAAGCAT 254  
Db 1432634 GTCTCCAAAGCAGCAGACCGGACCCACCGTGTGTGTCAGCGCAGGCGCGCTTT 1432575  
QY 255 GTACGACGACACGCCCATCTGGTCAAGGGCCACCGCTTGACACACCGCCTTTGACAA 314  
Db 1432574 CTTGCCGATTCCCGGTTGTGCGGTACGCCATGCCCGACCGATGGTCAGCTGGAACA 1432515  
QY 315 GATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCA 374  
Db 1432514 GCTCGCAAGACTTCGATGAAGTGCAGAACGCCATCGCCATCAAGAAAGGCGGATTCCTCA 1432455  
QY 375 GCAGCGCCGCGAGTGGTGGAGTCCACCGCGACGAAATTTGACTTNCACCAAC 429  
Db 1432454 GACCACCGAAGCCGTGCAGAAAGCCATGCCAAAGCTCATGACGCGGACCTAC 1432400

## RESULT 6

US-10-437-963-94550  
; Sequence 94550, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 94550  
; LENGTH: 548  
; TYPE: DNA



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; SEQ ID NO 32038
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-369-493-32038

Query Match
  7.7%; Score 46.2; DB 7; Length 1209;
Best Local Similarity 55.2%; Pred. No. 0.0012;
Matches 90; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 248 GAAGCATGTACAGCAGCACACCCCATCTGGTCAAGGGCCACGGCTTGACACCGCCACT 307
DB 86 GCACCTGCTCTTCGACGAAGTGTGTGGTGGAGCGCCGCGGAGGACACACCTGT 145

QY 308 TTGACAAGATCAACAGTACCTTGAGAGAGCGTGAAGAGATGGCGTCAAGCAGATG 367
DB 146 TCGTCCAGCTCTCGGGGACCGGGGGTGACCGTGCATGAATTCGGCAGCCTGCTCGCG 205

QY 368 TGATCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGACGA 410
DB 206 AGACTCTGCATCTCCCGAGCGAAGAGTTTCATCTCGACGA 248

RESULT 10
US-10-411-910A-264
; Sequence 264, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-910A-264

Query Match
  7.7%; Score 46.2; DB 9; Length 1509;
Best Local Similarity 46.2%; Pred. No. 0.0013;
Matches 153; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 54 CGGCGCGCAAGAAGCTGTTGATGACCTGGCGCGCAGAAAGGATGAAGCTGGCGTTGA 113
DB 846 CGGCGCGCAGCGCTGCAGCGCGACAGATCGCCCTCGACAGCAGCTGGCGGCGG 905

QY 114 CACCTTCTAGATAAGTGTGCTGACCGGAGCTGCTGCCCTTCTTCAGTCCCTGGA 173
DB 906 CGGCGAGATCGCCCGCATCATGAGCAGGCGGCGACCTGAGCGTGGCGACCGCCGTTGA 965

QY 174 CATGCAAGAGCAGAAAGTGAAGCAGGTCAAGTTTCATGAGCTTCGTTTCGCGGAGCAGA 233
DB 966 CACCTGTTTCGCGGACTGAAAGAGGACAAAGTGAACCGCCACAGCGGCCACAGCAGCGA 1025

QY 234 CCAATCAAGGCGCGAAGCATGTACGACGACACCGCCATCTGTTCAAGGGCCACCGCCT 293
DB 1026 CGGCCACCTGGCCACATCTTCGCCACGCGCCCAAGGAGCTGTTCAACGAGGACGTGA 1085

QY 294 GGAACACCGCCACTTTGACAAGATCAAGCATGATCTTGGAGAGACGCTGCAAGAGATGGG 353
DB 1086 GGAAGGTGACCTACCGCGCCCTTGGCGCAACAGGACTTCAGGAGGTGACCTGGGAAGAA 1145

QY 354 GPTCAAGCAGGATGTGATCCAGCAGCGCCG 384
DB 1146 CGGCGAGGTGCTGCTGCGCTTCGCGCGCCG 1176

RESULT 11
US-10-437-963-69229
; Sequence 69229, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363/c
US-10-437-963-97363/c
; Sequence 97363, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
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; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95374C.1
US-10-437-963-97363

Query Match
Best Local Similarity 7.6%; Score 45.2; DB 8; Length 2238;
Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 216 CGTGTTCGGGAGCAGACCAATACAAAGGCGCGAAGCATGTACGACGACACGCCCATCT 275
DB 1249 CGTGTTCGGGAGCAGACCAATACAAAGGCGCGAAGCATGTACGACGACACGCCCATCT 1190

QY 276 GGTCAAGGCGCAGCGCTCGACACCGCCACTTTGACAAGATCAAGCAGTACTCTTGAGA 335
DB 1189 GCCTATGCTCCAGATGCTCAACTTACCGAGGCGCTGCCATGACGACGCGCCGCA 1130

QY 336 GAGGCTGAAGAGATGGCGGTCAAGCAGGATGTATCCAGCAGCGCGCGGAGTGTGA 395
DB 1129 GAAGCTCTTCAAGGTGCTCGACATGTACGAGGCGGTCCGCGACGCGCGCGTCA 1070

QY 396 GTCCACCGCGCAGCAATTTGACTTNCACCAACTGCGC 434
DB 1069 CGCTTCATCGCGCGCTGCTCCACCAAGCGCGCGCGC 1031

RESULT 13
US-10-502-351-1
; Sequence 1, Application US/10502351
; Publication No. US20050155088A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Lian Hui
; APPLICANT: Lin, Yi Han
; APPLICANT: Xu, Jin Liang
; TITLE OF INVENTION: Ralstonia AHL-Acylase Gene
; FILE REFERENCE: 2977-154
; CURRENT APPLICATION NUMBER: US/10/502,351
; CURRENT FILING DATE: 2004-07-23
; PRIOR FILING DATE: PCT/SG02/000011
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 3743
; TYPE: DNA
; ORGANISM: Ralstonia sp.
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is a, c, g, or t
US-10-502-351-1

Query Match
Best Local Similarity 7.6%; Score 45.2; DB 10; Length 3743;
Matches 164; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 69 GTTTCATGACCTTGGGCGCGCAGAAAGGATGAAGCTGGCGGTTGACACCTTCTACGATAA 128
DB 2055 GCTCAGCTGATGGCGGCTCGATCGCGCCTTCCCGGTGGTGAGCATCGGCTTCAACAA 2114

QY 129 GGTGCTGCTGACCGCGAGCTGCTGCTCTTTCAGTCCCTGGACATGCAAGACAGAA 188
DB 2115 GGACGTGGTGAGCGACACCGTCTCCACCGCGCGCGCTTTCACCTTGTTCGAACCTGAA 2174

QY 189 GATGAAGCAGGTTCAAGTTTCATGAGTTTCGTGTTGGCGGAGCAGACCAATACAGGGCGG 248
DB 2175 GCTGCCGAGGCGACCGGACCACTTACTGTGACGCGACCGCGCAACAGATGACCAC 2234

QY 249 AAGCATGTACGACGACACCGCCCATCTGTGTAAGGGCCACCGCCTGGACCACTT 308
DB 2235 CGCAGCGTTCGCTTCGAGCTCAAGCTGCGGACGCGCGCTCGAGCGCGCACAC 2294
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QY 309 TCACAAGATCAAGCAGTACTTGGAGAGACGCTGCAAGAGATGGCGGTCAAGCAGATGT 368
DB 2295 CTTCTACGACACCATCTACGCGCGGTCTGTGATGCGGCGGCGCATGCGCTGGAC 2354

QY 369 GATCAGCAGCGCGCGGAGTGGTGGAGTCCACCGCGCAGCAATTTGACTTNCACAA 428
DB 2355 CACGAGAAGGCGCTACGCGCTTGGCGAGCGCAACCGCAACACACGCGCTCGGTGACAG 2414

QY 429 CTG 431
DB 2415 CTG 2417

RESULT 14
US-10-437-963-35783
; Sequence 35783, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 35783
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39672C.1
US-10-437-963-35783

Query Match
Best Local Similarity 7.4%; Score 44.4; DB 8; Length 1445;
Matches 141; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 139 GACCCGGAGCTGTGCTCCCTTCTTCAGTCTCCCTGGACATGCAAGAGCAGCAAGATGAAGCAG 198
DB 167 GACCGCTCGCAGCTGGCGGACGACCTCGACCGGAGCTCGCGGAGCTCGAGCCCAAGCTG 226

QY 199 GTCAAGTTTCATGAGCTTGTGTTGGCGGAGCAGACCAATACAAAGGCGCGGAGCATGTAC 258
DB 227 GCCCAGCTGGCGCGCGCGGCAACCGCGGCTGCTCCAGGTGCGACCGCTGTACGAGGAC 286

QY 259 GACCCACACGCCCATCTGTTCAAGGCGCAGCGCTGGACCAACCGCCACTTTTGACAAGATC 318
DB 287 GACCGGTGAGCGACATGTTGATGACCTTGTCTCCGGCCCCGACCTCTCGACTGATGATC 346

QY 319 AAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGCAC 378
DB 347 CGCTCCGCGCGCGCGCGCTCCGCGAGCGCTCGCGCGCGCTCGTCCGCGAGCTC 406

QY 379 GCGCGCGAGTGTGGAGTCCACCGCGCAGCAATTTGACTTNCACCAACTGGGACCC 438
DB 407 GCGGAGCGCTCGCGCACTGCGACCGCGCGGGGTGCGCCACCGCGAGCTCAAGCCGAC 466

QY 439 AAC 441
DB 467 AAC 469

RESULT 15
US-10-389-566-49/c
; Sequence 49, Application US/10389566
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; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-389-566-49

Query Match          7.4%; Score 44.2; DB 8; Length 1000;
Best Local Similarity 53.8%; Pred. No. 0.005;
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 66 GCTGTTTGATGACCTGGCGGCGCAGAGGATGAAGCTGGGGGTTGACACCTTCTACGA 125
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
676 GCAGTTTCATCGCGCGGTCCACGCCGCGGAGATGCTCAGCGTAGAGGGCTACCAACGA 617
QY 126 TAAGTGCTGGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGACGA 185
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
616 CATCGTGTGGCGGCGGAGGAGCGCTGTCCGCCGCGGAGATCCTGGGTTGACACGCCCC 557
QY 186 GAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGAC 234
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
556 GACGCTCAAGAGTCGGAGGAGTGGCGCGCGTGGTGTTCGTCGCCGAC 508

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Search completed: August 12, 2006, 08:39:19  
Job time : 1187 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length				
C	1	47.4	7.9	1781	6	US-10-449-902-20040	Sequence 20040, A
	2	47	7.9	1830	6	US-10-449-902-7207	Sequence 7207, Ap
	3	47	7.9	2261	6	US-10-449-902-25898	Sequence 25898, A
C	4	44.2	7.4	898	8	US-11-266-748A-371178	Sequence 371178, A
	5	44.2	7.4	898	8	US-11-266-748A-454557	Sequence 454557, A
	6	44.2	7.4	2559	9	US-11-218-305-13889	Sequence 13889, A
C	7	44	7.4	1676	6	US-10-449-902-10126	Sequence 10126, A
	8	44	7.4	1770	6	US-10-449-902-20915	Sequence 20915, A
	9	43.8	7.3	1451	6	US-10-953-349-29115	Sequence 29115, A
C	10	43.8	7.3	1451	9	US-11-056-355B-68882	Sequence 68882, A
	11	43.2	7.2	3618	9	US-11-218-305-17353	Sequence 17353, A
	12	42.6	7.1	3487	8	US-11-266-748A-57192	Sequence 57192, A
C	13	42.2	7.1	1467	6	US-10-449-902-7212	Sequence 7212, Ap
	14	42	7.0	1052	6	US-10-902-902-15213	Sequence 15213, A
	15	41.6	7.0	575	8	US-11-266-748A-3647	Sequence 3647, Ap
C	16	41.6	7.0	575	8	US-11-266-748A-63159	Sequence 63159, A
	17	41.6	7.0	575	8	US-11-266-748A-65991	Sequence 65991, A
	18	41.6	7.0	719	8	US-11-266-748A-7273645	Sequence 7273645, A
C	19	41.6	7.0	719	8	US-11-266-748A-334162	Sequence 334162, A
	20	41.6	7.0	807	8	US-11-266-748A-76043	Sequence 76043, A
	21	41.6	7.0	807	8	US-11-266-748A-109209	Sequence 109209, A
C	22	41.6	7.0	807	8	US-11-266-748A-128854	Sequence 128854, A
	23	41.6	7.0	1000	8	US-11-266-748A-286931	Sequence 286931, A



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Query Match
Best Local Similarity 7.4%; Score 44.2; DB 8; Length 898;
Matches 103; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 GCGCTGCTTCAGACGCGCCACACAGAGAGCGCGGAGCGGATGCGGGCGC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 GTGGTGCCACCGCGTGGCGCGCCAGCGCGAGCTGCTGGTGGGTGCGGGCCC 128
QY 61 AAGAAGCTGTTTGTATGACCTGGCGCGCGAGAGCATGAAGCTGGCGTTGACACCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
129 GAGCTGGGCGGTGGAGCGCGCGCTGCTGCTGAGCGCGCGCGCACCGCGCGC 188
QY 121 TACGATAAGTGTCTGGCTGACCGCGAGTGTGCTTCTTCTGAGTCTCCCTGACATGCAA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 GCGAGCGGGCCCTGGCGCTGAGAGCGCGGCGCTGCTGGGAGGTGGAGCTGGCG 248
QY 181 GAGCAGAAGATGAACAGGTC 201
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 GCCGAGGAGCGCGCGCAGGAC 269

RESULT 5
US-11-266-748A-454557/c
; Sequence 454557, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454557
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-454557

Query Match
Best Local Similarity 7.4%; Score 44.2; DB 8; Length 898;
Matches 103; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 GCGCTGCTTCAGACGCGCCACACAGAGAGCGCGGAGCGGATGCGGGCGC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
830 GTGGTGCCACCGCGTGGCGCGCCAGCGCGAGCTGCTGGTGGGTGCGGGCCC 771
QY 61 AAGAAGCTGTTTGTATGACCTGGCGCGCGAGAGCATGAAGCTGGCGTTGACACCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
770 GAGCTGGGCGGTGGGAGCGCGCGTGGCTGCGCTGAGCGCGCGCGCACCGCGCG 711
QY 121 TACGATAAGTGTCTGGCTGACCGCGAGTGTGCTTCTTCTGAGTCTCCCTGACATGCAA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
710 GCGACGGGCGCTGGCGCTGAGAGCGCGGCGCTGTGGCTCGGGAGGTGGAGCTGGCG 651
```

```
QY 181 GAGCAGAAGATGAAGCAGGTC 201
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
650 GCCGAGGAGCGCGCGCAGGAC 630

RESULT 6
US-11-218-305-13889
; Sequence 13889, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13889
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-13889

Query Match
Best Local Similarity 7.4%; Score 44.2; DB 9; Length 2559;
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 66 GCTGTTTGTGACCTGGCGCGCCAGAGCATGAAGCTGGCGTTGACACCTTCTACGA 125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1434 GCAGTTCATCGCCGCGTCCACGCGCGCGAGATCTCACGGTAGAGGCTTACCACGA 1493
QY 126 TAAGGTGCTGCTGACCCGCGAGCTGTGCTGCTTCTTCGAGTCCCTGGACATGCAAGAGCA 185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1494 CATCGTGTGCGCGAGCGCGTGTGCGCGCGAGATCTCTGGTTGCGCGGCC 1553
QY 186 GAAGATGAAGCAGGTCAAGTTTCATGAGCTTCTGTTGGCGGAGCAGAC 234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1554 GAGCTCAAGAGTCGAGGAGGTGGCGCGTGGTGTCTGTCGCCGAC 1602

RESULT 7
US-10-449-902-10126/c
; Sequence 10126, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10126
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107474
; DATABASE ENTRY DATE: 2002-08-28
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OTHER INFORMATION: Ceres Seq. ID no. 13655338  
US-11-056-355B-68882

Query Match 7.3%; Score 43.8; DB 9; Length 1451;  
Best Local Similarity 56.2%; Pred. No. 0.04;  
Matches 81; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 285 CCAGCGCTCGACACCGCCACTTTCAGCAAGATCAAGCAGTACCTTGGAGAGACCTGCA 344  
DB 291 CTTGCGCTCCGAGTCCGCGGACCTCGCTGACCGCCGACCGCTGGCGTGGAGAGATCCTGCG 350  
QY 345 AGAGATGGCGCTCAAGCAGGATGTATCCAGCAGCCCGCGAGTGGTGGATCCACCG 404  
DB 351 CGAGATCGCGCTCAAGTTCGCGGAGATCCAGAACGAGGCGCTCGGGGAGACCGGCTCCG 410  
QY 405 CGACGAATTTGACTTNNCCACAA 428  
DB 411 AGACCTCAACGACGAGATCAACAA 434

## RESULT 11

US-11-218-305-17353  
; Sequence 17353, Application US/11218305  
; Publication No. US2006014195A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaoid, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; TITLE OF INVENTION: Corr.  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 17353  
; LENGTH: 3618  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1640)..(1640)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1733)..(1733)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1885)..(1885)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1908)..(1908)  
; OTHER INFORMATION: n is a, c, g, or t

## US-11-218-305-17353

Query Match 7.2%; Score 43.2; DB 9; Length 3618;  
Best Local Similarity 46.9%; Pred. No. 0.084;  
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 2 CGCTGCTCGACAGCGGCCACACGACACACAGAGCGCGGAGCGGATGCGGGCGCA 61  
DB 2652 CGCGCGCGCGTACCGGAAGAACCGTTCACGCGCGCGGAGCGCGGAGGAGCA 2711  
QY 62 AGAAGCTGTTTGATGACTCGGGCGCGCAGAGGATGAAGCTGGCGGTTTGACACTTCT 121  
DB 2712 ATATAGGCGGAGGAGCTCAGGAGGAGGAGGCGCTGTACGTGAAGGTGAGCATGA 2771  
QY 122 ACGATAAGGTGCTGGTGCACCGGAGCTGTCTTCTTCGAGTCCCTGGACATGCAAG 181

DB 2772 GGGCGCCATACCTCCGAAGGTGACCTCGGACCTAGCGGCGGTACCGTGAAGCTGAGGG 2831  
QY 182 AGCAGAGATCAAGCAGGTCAAGTTTCATGAGCTTCGTTTGGGGGAGCAGACCAATACA 241  
DB 2832 ACGCGCTGGAGCGGCTCTTCGCTGCTTCCTCCTCGGCCGACGCGGAGATGCCAGTTTCG 2891  
QY 242 AGGCCGGAAGCATGTACGAGCGACACGCCCCCATCTGTGTCAGGGGCGCACG 289  
DB 2892 CCGTGCCTACGAGGACAAAGGACGCGGACCTCATGCTCGCGGCGGACG 2939

## RESULT 12

US-11-266-748A-57192  
; Sequence 57192, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 57192  
; LENGTH: 3487  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

## US-11-266-748A-57192

Query Match 7.1%; Score 42.6; DB 8; Length 3487;  
Best Local Similarity 50.7%; Pred. No. 0.12;  
Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 GCCTGCTCTGACAGCGCGCCACACAGACACGCGGAGCGGAGCGGATGCGGGCGC 60  
DB 379 GTGGTCCACCGCGCGCTGGCGCGCGCGCGGAGCTGTGTGTGGGGTTCGCGGCC 438  
QY 61 AGAAGCTGTTTTCATGACCTGGCGCGCGCAGAGGATGAAGCTGGCGGTTGACACCTTC 120  
DB 439 GAGCTGGGGCGTTGGGAGCGCGCGGCTGCGCTGAGGCGCGCGCGCGCGCGCGG 498  
QY 121 TAGCATAAAGTGTGCTGCTGACCGGAGCTGTCCCTTCTTCGAGTCCCTGGACATGCAA 180  
DB 499 GGGCAGCGGCGCTTGGCGCTGAGGAGCGCGGCTGTGGCTCGGGAGGTGAGCTGGCG 558  
QY 181 GAGCAGAAAGATGAAGCAGGTC 201  
DB 559 GCGGAGGAGCGCGCGCAGGAC 579

## US-11-266-748A-57192

Query Match 7.1%; Score 42.6; DB 8; Length 3487;  
Best Local Similarity 50.7%; Pred. No. 0.12;  
Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 GCCTGCTCTGACAGCGCGCCACACAGACACGCGGAGCGGAGCGGATGCGGGCGC 60  
DB 379 GTGGTCCACCGCGCGCTGGCGCGCGCGCGGAGCTGTGTGTGGGGTTCGCGGCC 438  
QY 61 AGAAGCTGTTTTCATGACCTGGCGCGCGCAGAGGATGAAGCTGGCGGTTGACACCTTC 120  
DB 439 GAGCTGGGGCGTTGGGAGCGCGCGGCTGCGCTGAGGCGCGCGCGCGCGCGCGG 498  
QY 121 TAGCATAAAGTGTGCTGCTGACCGGAGCTGTCCCTTCTTCGAGTCCCTGGACATGCAA 180  
DB 499 GGGCAGCGGCGCTTGGCGCTGAGGAGCGCGGCTGTGGCTCGGGAGGTGAGCTGGCG 558  
QY 181 GAGCAGAAAGATGAAGCAGGTC 201  
DB 559 GCGGAGGAGCGCGCGCAGGAC 579

## RESULT 13

US-10-449-902-7212  
; Sequence 7212, Application US/10449902

Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7212  
LENGTH: 1467  
TYPE: DNA  
ORGANISM: Oryza sativa  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: AK064340  
DATABASE ENTRY DATE: 2001-12-06  
US-10-449-902-7212

Query Match  
Best Local Similarity 7.1%; Score 42.2; DB 6; Length 1467;  
Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 285 CCAGCGCTCGACACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGAGCGCTGCA 344  
DB 224 CTTGCTCCGAGTGGCGCGACCTCGCGAGCGGCTCGGAGATCTCCG 283  
QY 345 AGAGATGGGGTCAAGCAGGATGTATCCAGCAGCGCGGAGTGTGGAGTCCACCG 404  
DB 284 CGAGATCGCGCCAGGTGCGCGAGATCCAGACGAGGCTCGGAGACCGCTCCG 343  
QY 405 CGAGCAATTTGACTTCCCAACAA 428  
DB 344 CGACCTCAACGACGAGATCAACAA 367

RESULT 14  
US-10-449-902-15213  
Sequence 15213, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15213  
LENGTH: 1052  
TYPE: DNA  
ORGANISM: Oryza sativa  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: AK065744  
DATABASE ENTRY DATE: 2001-12-06  
US-10-449-902-15213

Query Match  
Best Local Similarity 7.0%; Score 42; DB 6; Length 1052;  
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 162 CGAGTCCCTGGACATGCAAGAGCAGAGATCAAGCAGTCAAGTTCATGAGCTTCGTGTT 221  
DB 610 CAACTACTCACTACACACGCGGTGATGAAGCTGTCAAGTTCGGCGCTCGTCGG 669  
QY 222 TGGCGGAGCAGACCAATACAAAGGCCGCAAGCATGTAGACGACACGCCCATTTGGTCAA 281  
DB 670 CTACGACAAACACGCTCTGGAACGCTCCGTCTCCGCGCGACGCCCATATGCGCAA 729  
QY 282 GGGCGACGGCTGGACACCGCCACTTTGACAAGATCAAGCAGTACCTTG 331  
DB 730 GTATATCCGCTACTACCGGACCTTGTGTCGAGCTCAACAAGGCCCTCG 779

RESULT 15  
US-11-266-748A-3647/c  
Sequence 3647, Application US/11266748A  
Publication No. US20060134663A1  
GENERAL INFORMATION:  
APPLICANT: Harkin, Paul  
APPLICANT: Johnston, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
TITLE OF INVENTION: Methods of Using the Same  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266,748A  
CURRENT FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3647  
LENGTH: 575  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (530)..(530)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (543)..(543)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-3647

Query Match  
Best Local Similarity 7.0%; Score 41.6; DB 8; Length 575;  
Matches 89; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 266 ACGCCCATCTGGTCAAGGCGCACGGCTTGACACCGCCACTTTGACAAGATCAAGCAGT 325  
DB 194 ACCTACTCAGGCGCAGCGGCTTCTGCTGGCGCAGTCTCACTGGAGCAGCGGAGT 135  
QY 326 ACCTTGGAGAGCGCTGCAAGAGATCGGCGTCAAGCAGGATGTGATCCAGCAGCGCCG 385  
DB 134 CGGTGGCGGCAACGCGCAGCAAGATCGGCTTCGGCATCTGCTCAGCAAGGAGCCGACG 75  
QY 386 GAGTGTGAGTCCACCGCGAGCAATTTGACTTCCCAACTGGCG 434

Db 74 GCGTGTGGGCGCTACAAACCGCGGGGAGCACCCCATCTTTCGTCAACTCCCC 26

Search completed: August 12, 2006, 08:42:21  
Job time : 187 secs



1	232	20.7	126	2	US-09-902-540-13031	Sequence 13031, A
2	136	12.1	345	2	US-09-252-991A-32377	Sequence 32377, A
C 3	134.5	12.0	170	2	US-09-252-991A-19980	Sequence 19980, A
C 4	134	11.9	663	2	US-09-252-991A-30843	Sequence 30843, A
C 5	130.5	11.6	308	2	US-09-252-991A-37249	Sequence 37249, A
C 6	129	11.5	1476	2	US-09-252-991A-29427	Sequence 29427, A
C 7	136	11.2	235	2	US-09-252-991A-24046	Sequence 24046, A
C 8	125.5	11.2	394	2	US-09-252-991A-19344	Sequence 19344, A
C 9	134	11.1	312	2	US-09-252-991A-19787	Sequence 19787, A
10	132	10.9	726	2	US-09-252-991A-20675	Sequence 20675, A
11	121.5	10.8	204	2	US-09-252-991A-17837	Sequence 17837, A

[illegible]

## RESULT 2

US-09-252-991A-32377  
; Sequence 32377, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Alignment Scores:	
Pred. No.:	8,97e-06
Score:	136.00
Percent Similarity:	34.8%
Best Local Similarity:	30.4%
Query Match:	12.1%
DB:	2
Length:	345
Matches:	70
Conservative:	10
Mismatches:	64
Indels:	85
Gaps:	10

US-09-920-953-2 (1-598) x US-09-252-991A-32377. (1-345)

539	Qy	CAGGCTCTCGGGCCCGCTGGGCGCGCTCGGCAACTGGCGTCCCC---	GTCATAATCGA	483
101	Db	GlnGlyProGlyGlyProGlyArgAspArgGlnValArgLeuProAlaAlaProGlyArg	120	
482	Qy	TGGAATCAGCGCTCAGGCTGGGGTTGGGTTAATGAAATCAGTTGGGTGCGCGAGTTGTG	423	
		:::		
121	Db	ProSerArgArgGln-	SerArgLeu	128
422	Qy	GGNAATCAAAATTCGTCGGCGGTGACTCCACCACTCGGCGCGTCTCGA	371	
		:::		
129	Db	GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgArgProSerProAla	148	
370	Qy	-----	TCACATCC	363
148	Db	atTpArgGlnProProIleGluLeuGlyAlaValArgLeuArgProGlnArgArgP	168	

[illegible]

### RESULT 3

```

US-09-252-991A-19980
; Sequence 1980; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

Alignment Scores:	9.92a-06	Length:	170
Pred. No.:	134.50	Matches:	68
Score:	38.3%	Conservative:	9
Percent Similarity:	33.8%	Mismatches:	45
Best Local Similarity:	33.8%	Indels:	79
Query Match:	12.0%	Gaps:	15
DB:	2		

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)

Qy	524	CTGTGGCGGGCTGCGCAACTGGCGCTCCCGCTCAA-----AATCGATGGAATGAGCGC	471
Db	14	ProGlyIArgArgAsnArgAlaProAlaAlaAlaGlyArgArgSerAlaArg	33
Qy	470	TCAGCTCG-----GPTTGGTTTAATCAAAATCAGTTGGTCGCGAGTTGTTGGGNAAG	417
Db	34	SerGlyITrpProCysGlyITrp-----Arg-TrpSerHisProCysTrp-----	47
Qy	416	TCAAATTCGTGCGGGGTGGATCCACCACTCCGCGCGCGTGTGGATACATCCTGCTTG	357



Qy	437	GGTGGCGAGTTGTTGGGNAAGTCAAATTCTG	-----CGCGGTGGAGTCCACCACTCGG	384
Db	78	oValArgSerAlaCysArgGlyThrSerArgProValArgSerTrpProGlyProProAl	98	
Qy	383	CGCGGTCTCGATCACAATCTGCTTGACG	-----CCATCTCTTCG	342
Db	98	aGlyArgAlaGlyGlyTyArgArgArgGlyProArgArgSerValProProThrVa	118	
Qy	341	AGCGTCTCTCCAAGTACTGCTTGATCT	-----TGTCAAAGTGGCGGTGGTCC	294
Db	118	lAlaSerValAlaGlyProSerArgSerGlyAlaGlyProAlaAArgAlaAlaGlyPr	138	
Qy	293	AGCGGTGGCCCTTGACCA	-----	275
Db	138	oGlyAlaAlaProCysProGlyProGlyArgGlySerGlyAlaAlaArgArgHisArgAr	158	
Qy	274	-----CATGGCGTGGCTGCTACATGCTTCGGCCCTTGTATTGGTCTGCTCGG	225	
Db	158	gGlyArgArgProGlyArgArgSerArgTrpCys	---ProCysAlaGly---SerAr	175
Qy	224	CAAACACGAAGCTCATGAACCTTGACCTTCATCTTCTGCTCTTCGATGTCACAGGAC	165	
Db	175	gAlaArgArgProSer	-----GlyCysThrGlyCy	185
Qy	164	TCGA	-----AGAAGGCA-----GCAGTCCGGGTGACCCAGCACCTTA	126
Db	185	sArgProArgLeuProArgArgAlaGlyArgArgAlaAlaGlyGlyArgProPro	-----203	
Qy	125	TCGTAGAAGGTGTCAACCGCCAGCTTTCATGCTTCTGCGCGCCAGGTTCATCAA	-----71	
Db	204	-----CysCysProProGlyAla	-----ProGlyGluArgGlySer	215
Qy	70	-----ACAGTCTTTCGCGCCGCATCCCGCTTCGCGCTCTGTGTGGTCTGGTGC	CGCG	15
Db	215	gSerThrGluSerSerAlaArg	---ProAlaProArgProCysGlyGlySerGlyArgG	234
Qy	14	TCTCGACGCAGCGC	1	
Db	234	lyAlaArgHisArg	238	

## RESULT 6

US-09-252-991A-29427  
; Sequence 29427, Application US/09252991A

```

; Sequence 29421, Application 05/0522991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

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, FILE REFERENCE NUMBER: 10198-136
, CURRENT APPLICATION NUMBER: US/09/252,991A
, PRIOR FILING DATE: 1999-02-18
, CURRENT APPLICATION NUMBER: US 60/074,788
, PRIOR FILING DATE: 1998-02-18
, CURRENT APPLICATION NUMBER: US 60/094,190
, PRIOR FILING DATE: 1998-07-27
, NUMBER OF SEQ IDS NOS: 33142

```

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; SEQ ID NO 29427
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29427

```

Alignment Scores:		
Pred. No.:	8.64e-05	1476
Score:	129.00	74
Percent Similarity:	33.5%	10
Best Local Similarity:	38.0%	Conservative:
Query Match:	11.5%	Mismatches:
DB:	2	Indels:
		Gaps:

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

Qy	9	TGCAGACGGCCGACACAGCACACCGCGGAAGC-----GGGNTGGG	56
Db	492	CysArgAlaHisArgGlnHisArgArgGlnAlaAlaAspAlaLeuGlyGln	511
Qy	57	GCGCACAAAGCTGTTTCATCACTGGCGCGCGCAAGAGGCATGAAGCTGGCGGTTGCAC	116
Db	512	ThrGlnLeuSerArg---ArgProGlyGlnLeuArgAlaProGlyHisArgAlaHis	530
Qy	117	CTTCTACGATAAGTGTGCTGACCCGAGAGCTGCTCCCTCTTCGAGTCCCTGGACAT	176
Db	531	LeuProGlnLeuGlyAlaAla---ValGlyGlyAlaGlyLeuArgArg-----GlyHis	547
Qy	177	GCAAGACGACGAAGATGAAGCAGGTCCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGCA	236
Db	548	ArgProGlyArgTrpProValGlyLeuValArg-----ArgArgLeuPro	562
Qy	237	ATA-----CAAGCGCGAAGCATGTACGACGACACGCCCATCTGTCACAGGGCCACGG	290
Db	563	AlaGlyArgArgGlyThrArgArgGlnGlyArgThrArgArgProGlyProGlyProAla	582
Qy	291	CTGTGA-----CCACCGCCA-----CTTTCACAAGATCAAGCAGTA	326
Db	583	ProGlyAlaGlyAlaAspAspArgProProProAlaPheLeuLeuSerGlyAlaAlaArg	602
Qy	327	CTTTGGAGACGCTGCAAGAGATGGCGCTCAA-----GCAGATGTGATCCAGCAGCG	380
Db	603	Pro---ArgArgAlaGlyProAspAspArgGlnProProAlaGlyProAspProGlyArg	621
Qy	381	CGCGGAGTGGAGTCCACCCGC-----GACGAATTGACTTTCACCAACA	428
Db	622	ArgHisArgGlyAlaVal-ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr	641
Qy	429	CTGGGCACCAACTGATTTCATTAAACCAACCCAG-----465	
Db	641	oProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi	661
Qy	466	----CCTGACGGCTTCCTCCATCATGTTTGGCGGGAGCGCCAGTTCGCCAGCGCGCCC	521
Db	661	sProProGlyArgAspAlaArg-----AlaThrValArgProArgPr	676
Qy	522	AGGGGGCCAGGAGCCCTGCAAAATCGTTTGGCAGCCCTTGCTGCATTAAGAGCCATCAG	580
Db	676	oSerArgProAlaGly-GlnTrpHisProProAlaAlaArgValAlaGlyAlaGlyArgHisArg	695

## RESULT 7

US-09-252-991A-24046  
; Sequence 24046, Application US/09252991A

```

sequence 21070; application 00/022322.0001
;
; Patent NO. 6551795
;
; GENERAL INFORMATION:
;
; APPLICANT: Marc J. Rubenfield et al.
;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

```

;  
 ; TYPE: PRT  
 ; ORGANISM: *Pseudomonas aeruginosa*  
 US-09-252-991A-24046

Alignment Scores:	9.02e-05	235
Pred. No.:	136.00	47
Score:	33.2%	Matches:
Percent Similarity:	28.3%	Conservative:
Best Local Similarity:	11.2%	Mismatches:
Query Match:	2	Indels:
DB:		Gaps:

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US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)
QY 482 TGGATGAGCGCTCAGGC---TGG-----GGTTGGTAAATAAATCAG 441
Db 26 TrpAspGlyArgSerGlyArgTrpSerArgArgTrpCysAlaTrp----- 40
QY 440 TTGGGTGCGCAGCTTGTGGNAAGTCAAAATTCGTCCGGGTGAGCTCCACCACTCCGGCG 381
Db 41 ---GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
QY 380 GCGTCTCGATCACAATCTGCTGTGACGCCCATCTCTTGACAGCGTCTCTCCAGGTTACTGC 321
Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer----- 77
QY 320 TTGATCTTGTCAAGTGGGGTGTCCAGCGCGTTCAGCCCTTGACAGATGGCGGTGTCG 261
Db 78 -----ArgArgTyThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
QY 260 TCGTACATGCTCGGCCCTTGTATTGGTCTGCTCCGCCAAACACCAAGCTCATGACTTG 201
Db 92 -----ThrProProPro---Thr----- 96
QY 200 ACTGCTTCATCTTCTGCTTGTGATGTCAGGGACTCGAAGAGGGCAGCGCTCCGGG 141
Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerLysHisAlaAlaProGl 114
QY 140 TCAGCCAGCACTTATCCTAGAGTGT-----CAACGCCAGCTTCATGCGCT 93
Db 114 yValSerAlaSerAlaSerAlaAlaArgCysAlaCysSerSerProGlySerSerGlyGl 134
QY 92 TCTGCGCGCCCGAGTCAATCAACAGCTTCTTGGCGCGCATCCGCTTCCGCGTCTCT 33
Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153
QY 32 GTGGTGTGCTGGCGG 17
Db 153 gTipProArgTrpPro 158

RESULT 8
US-09-252-991A-19344
; Sequence 19344, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19344
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19344

Alignment Scores:
Pred. No.: 0.000124 Length: 394
Score: 125.50 Matches: 68
Percent Similarity: 31.8% Conservative: 16
Best Local Similarity: 25.8% Mismatches: 76
Query Match: 11.2% Indels: 104
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19344 (1-394)
QY 17 CGGCCACGACCAACAGAGACGG-----CGG 43

```

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Db 116 ArgProGlyAlaProGluProArgGlyThrProProValGlyProGlySerLeuSerArg 135
QY 44 AAGCGGATCGCGCGCAAGAAGCTGTTGTATGATCACTGGCGG-----CGCAG 91
Db 136 ArgLysProAlaGly-AspLeuAla-----ProProArgGlnLeuAlaAspArgPr 152
QY 92 AAGCATGAAGCTGGCGGTTGACACCTTCTACGATAGGTGCTGCTGACCGGAGCTGC 151
Db 152 oAlaHisProProGlyGlySerHisLeuGlnLeuProGlyAlaGlyProProGlyArgVa 172
QY 152 T-----GCCCTTCTTCCA----- 164
Db 172 lArgProAlaValSerLeuProProAlaValPheArgArgLeuHisGlnProAlaValAr 192
QY 165 -----GTCCCTGACATCAAGACAGCAAGATGAAGCAGGTCAAGTTTCATGAGTTCG 217
Db 192 gArgProLeuProGlyHisAlaAla-----AlaGlyArgThrHisProGlnAl 209
QY 218 TGT-----TGGCGGACGACACCAT 238
Db 209 aValProProAlaLeuSerArgArgProAlaGlyAlaProGlyArgArgGlnProAs 229
QY 239 ACA-----GGCGCGAAGCATGTACGACGACACGCGCATCTGTCAGGGCCAGCGCTCGG 295
Db 229 pGlnProAspProProAlaArgProArgLeuProAlaLeuAlaGlyProArgProGl 249
QY 296 ACCACGCCCACTTTGACAGATCAAGCATGACCTTTGGAGAGAGCTGCAAGAGATGGCG 355
Db 249 yArgProProThrAlaHisGluPheAlaAspProAlaThrProProAlaArgGlyArgAr 269
QY 356 TCAA----- 359
Db 269 gGlnLeuProAlaThrGlnGlyProProAlaAlaArgProGlyAspLeuProProGlySe 289
QY 360 ---GAGGATGTATCCAGCAGCGCGCGAGTGTGTGGAGTC----- 398
Db 289 rGlyArgAlaValAspProGlyHisArgArgAlaAlaArgLeuPheArgAlaLeuGlyLe 309
QY 399 -----CACCGCGCAGAAATTTGACTTTCNCCAACA 427
Db 309 uProSerArgValGlnGluValAspArgProHisProArgArgVal----- 324
QY 428 ACTGCGCACCACTGATTTTCAACCAACCCAGCTGAGCGCTCATTCCATCGAT 487
Db 325 -----ProAlaProGlyGlySerLeuLysLeuSerPr 335
QY 488 TTTGAGCGGGAGCGCAGTTGCGAGCGCGCCAGCGCGCCAGGAGCGCTGCAAAATCGT 547
Db 335 oThrProGlyAspGluAlaArgCysAlaValGlyArgAlaProTrpArgThrAlaAlaAl 355
QY 548 TTGCCAGGCC 557
Db 355 aAlaArgPro 358

RESULT 9
US-09-252-991A-19787
; Sequence 19787, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19787
; LENGTH: 312
; TYPE: PRT

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;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 17837  
;; LENGTH: 204  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17837

Alignment Scores:  
Pred. No.: 0.000258 Length: 204  
Score: 121.50 Matches: 60  
Percent Similarity: 34.6% Conservative: 15  
Best Local Similarity: 27.6% Mismatches: 77  
Query Match: 10.8% Indels: 65  
DB: 2 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

QY 5 TGCTGCAGACGGCGCCACACGAGCAGCGGCGGAGCGGATCGGCGCAAGA 64  
Db 7 CysSerSerThrArgProThrProThrTrp-----ProSerAlaasn 21  
QY 65 AGCTGTTGATGACCTGGCGGCGGAGAGGATGAAGTGGCGTTGACACCTTCTACG 124  
Db 22 SerMetAlaThrAlaTrpProPheProAlaAlaSerTrpArgThr-----Thr 39  
QY 125 ATAAGTGTGG-----CTGACCGGAGTGC-----151  
Db 40 SerArgCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59  
QY 152 TGCCCTTCTCGAGTCCCTGGACATCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGA 211  
Db 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProArgSerSer-----76  
QY 212 GCTTCGTGTTGGCGGAGCAGCAATACAAAGGCGGCAAGCATGTACGACGACACGCC 271  
Db 77 -----ArgGluProGluProCys-----ArgAlaPro 85  
QY 272 ATCTGTCAAGGCCACGGCTGAGCAGCCACCTTTGACAGATCAAGCAGTACTTG 331  
Db 86 ProTrpSer-----AlaAlaTrp-----AlaAlaThrCys 95  
QY 332 GAGAGCGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGCAGCGCGCGGAGTGG 391  
Db 96 ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp 109  
QY 392 TGGAGTCCACCGCGAGATTTGACTTNCACCAACTCGCAGCCCACTGATTTTCAT 451  
Db 110 ThrLeuProThrProGlySerAlaAlaAlaProAlaCysAlaSerGlyIle-----126  
QY 452 TAACCAACCCAGCTGAGCGCTCATTCATGATTTTGGCGGGGAGCGCCAGT---508  
Db 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProPro 143  
QY 509 -----GCCGAGCGCGCCAGGGGCCAGGAGCGCTGCAAAATCGT 547  
Db 144 ArgSerProArgGlyTrpSerGluSerMetArgTrpCysTrpGlnProAla-----161  
QY 548 TTCCAGCCCTTGTGTCATTGAAGAGCCATCAGCCATTTCGACCAAGCC 598  
Db 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgArgAla 177

RESULT 12  
US-09-252-991A-18476  
; Sequence 18476, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 18476  
;; LENGTH: 351  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18476

Alignment Scores:  
Pred. No.: 0.000317 Length: 351  
Score: 121.50 Matches: 58  
Percent Similarity: 33.5% Conservative: 10  
Best Local Similarity: 28.6% Mismatches: 58  
Query Match: 10.8% Indels: 77  
DB: 2 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)

QY 30 CACAGACGGCGGAGCGGATCGGCGGCAAGAGCTGTTGATGACCTGGCGGCGC 89  
Db 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArg 150  
QY 90 AGA-----AGGCATGAAGTGGCGGTTGACACCTTCTACGATAAGGT 131  
Db 151 LysProAlaValArgProAlaArgHisAlaAlaProAla-----163  
QY 132 GCTGCTGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGGA-----CATGCA 179  
Db 164 -----ProGlyLysAspProArgArgArgGlyAspGlnGluProHisArg 180  
QY 180 AGACAGAGAAGTGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGCAATA 239  
Db 181 AlaAlaArgArgArgAlaGlyGlyAlaHis-----ArgProTrpArg---ArgProLeu 197  
QY 240 CAAGGCGCGAAGCATGTACGACGACACGCCCATCTGTGTCAGGCGCCGCTGGACCA 299  
Db 198 ProGlyProAspHisProArgGlyGlnProAlaGlyLysLeuProHisAla-----215  
QY 300 CGCCCACTTTGACAAGATCAAGCATGACCTTGGAGAGACGCTGCAAGAGATGGCGTCAA 359  
Db 216 -----AlaIleArgArgGlyArgGln 222  
QY 360 -----GCAGGATGTATCCAGCA-----CGCCGCGCG 386  
Db 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg 242  
QY 387 AGTGTGGAGTCCACCGCGCAGCAATTTGACTTNCACCAACTGCGCAGCCCACTGATT 446  
Db 243 ProGlyAlaValAlaProAlaArgLeuGlyAsnLeuAlaGlyGlnAlaGln-----260  
QY 447 TTCAATTAACCCCAACCCCGCTGAGCGCTCATTCATCGATTTTGGAGCGGAGCGCCAG 506  
Db 261 -----GlyArgArgAla 264  
QY 507 TTGCGC-----AGCGCGCCAGGGGGCCAGGAGC 536  
Db 265 GlyProArgArgArgArgAlaAlaArgHisLeuArgProProArgArgProArgArg 284  
QY 537 CTGCAATC 545  
Db 285 LeuArgVal 287

RESULT 13  
US-09-252-991A-20161  
; Sequence 20161, Application US/09252991A

Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 20161  
 LENGTH: 248  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-20161

Alignment Scores:  
 Pred. No.: 0.000314 Length: 248  
 Score: 121.00 Matches: 47  
 Percent Similarity: 35.1% Conservative: 19  
 Best Local Similarity: 25.0% Mismatches: 62  
 Query Match: 10.8% Indels: 60  
 DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)

QY 2 CGCTGCTGCAGACGGCGCCACAGCA---CCACAGACGGCGGAAGCGGATCGGGC 58  
 DB 56 ARGCSyAlaArgSerProProAlaGlyProSerSerThrArgArgProAlaSer 75  
 QY 59 GCAAGA---AGTGTGTGATGACCTGGCGCGGCGAAGCATGAAGCTGGCGGTGACA 115  
 DB 76 AlaSerIleArgCys-----SerAlaArgValArgIleYsrTrpSerThr 90  
 QY 116 CTTTCTACATAGG----- 130  
 DB 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgTrpCysArg 110  
 QY 131 -----TGCTGGCTGACCCGGAGC-----TGCTGC----- 154  
 DB 111 ARGCSyAlaCysTrp---ThrArgAsnArgProAlaArgSerCysArgCysValAla 129  
 QY 155 -----CCTTCTCGAGTCCCTGGACATGC 178  
 DB 130 ThrArgSerSerAlaProProThrProProAlaProThrSerIleProThrProCys 149  
 QY 179 AAGACAGAGATGAAGCAGGTCAAGTTCATGAGCTTCTGTTGGCGGAGCAGACCAAT 238  
 DB 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla--- 159  
 QY 239 ACAAGGCGGAGCATGTACGACGACACGCGCCATCTGGTCAAGGCGCCAGCTGGACC 298  
 DB 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTrpArgSerAlaGlySerThrAla 178  
 QY 299 ACCGCCACTTTCACAAAGTCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATGGCGTCA 358  
 DB 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196  
 QY 359 AGCAGATGTGATCCAGACGCGCGGGAGTGGAGTCCACCGCGCAAGATTGTACT 418  
 DB 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216  
 QY 419 TNCCCAACAACCTGCCACCCCACT 442  
 DB 217 SerProSerAlaAlaGlnProSer 224

RESULT 14

US-09-252-991A-20509  
 Sequence 20509, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 20509  
 LENGTH: 686  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-20509

Alignment Scores:  
 Pred. No.: 0.000461 Length: 686  
 Score: 121.00 Matches: 51  
 Percent Similarity: 35.2% Conservative: 5  
 Best Local Similarity: 32.1% Mismatches: 47  
 Query Match: 10.8% Indels: 56  
 DB: 2 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)

QY 3 GCTGCTGCAGACGGCGCCACAGCA---CCACAGACGGCGGAAGCGGATCGGGCGCAA 62  
 DB 117 AlaAlaCysArgArgGlyAlaTrpHis-----GlyLeuArgProArg 130  
 QY 63 GAAGCTGTTTGCATGACCTGGCGCGCGCAGAAAGCATGAAGCTGGCGGTGACACCTTCTA 122  
 DB 131 ProAla-----GlyArgArgArgProAlaAlaGlyGly----- 142  
 QY 123 CGATAAGTGTGCTGACCGGAGCTGCTCCCTTCTTCGAGTCCCTGGACATGCAAGA 182  
 DB 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155  
 QY 183 GCAGAAGATGAAGCAGGTCAAGTTCATGAGCTTCTGTTTGG----- 224  
 DB 156 ProAlaProArgThr-----ValAlaArgArgArgProTrpArgHisProArgCysAla 173  
 QY 225 -----CGAGACAGCAACATCAAGGCGCGGAGCATGTACGACGACACGCCCATCTGCT 278  
 DB 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgGlyAlaGly 191  
 QY 279 CAAGGCGCACGGCTGGACACCGCCACTTTGCAAGATCAAGCAGTACCTTGGAGAGAC 338  
 DB 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205  
 QY 339 GCTGCAAGA-----GATGGCGGTCAA 359  
 DB 206 AlaAlaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225  
 QY 360 GCAGATGTGATCCAGACGCGCGCGGAGTGGTGA-----GTCCACCCG 404  
 DB 226 ProGlyAlaGlyAlaGlyProArgArgGlyGlyGlyValaArgArgThrHisPro 244

RESULT 15

US-09-252-991A-23215  
 Sequence 23215, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18



; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23215  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23215

Alignment Scores:  
Pred. No.: 0.000383 Length: 219  
Score: 120.00 Matches: 57  
Percent Similarity: 38.1% Conservative: 18  
Best Local Similarity: 29.1% Mismatches: 72  
Query Match: 10.7% Indels: 49  
DB: 2 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-23215 (1-219)

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Qy 593 GGTGCGAAATGGCTGATGGCTTCAATGCGAAGGGCTGGCAACGATTTCAGGCT 534
Db 58 GlyArgArgTyrSerAspArgSerAlaPro-----AlaAsnProProGly 73
Qy 533 CCTGGGCCCCCTGGCGGCTGCGCAACTGCGCTCCOC-----GCTCAAAATCGA 483
Db 74 ProGlySerValProArgSerArgArgTyrAlaValProGlyAlaAlaArgSerArg 93
Qy 482 TGAATGAGCGCTCAG-----GCTGGGTTGGGTTAATGAAATCAGTTGGGT 435
Db 94 -ProAlaThrGlyProProArgTyrAlaGlyProGlyHisArgAlaAlaAlaTyrLe 113
Qy 434 GCGCAGTTGTTGGGNAAGTCAAAATTCGTCGGGGTGGACTCCACCACTCCGGCGGCGTGC 375
Db 113 uArg-----ArgArgAlaSe 118
Qy 374 TGGATCACATCTGTTGACGCCCATCTCTTGACGGCTCTCCAAAGTACTGCTTGATC 315
Db 118 rAlaSerCysProGlyHisArgArgGlyAspSerGlySerSerProGlyProArgLysAl 138
Qy 314 TTGTCAAAGTGGCGGT-----GGTCCAGGCGGTGGCCCTTACCCAGATGGCGGTGT 264
Db 138 aThrArgGlyHisGlyArgLysArgProProGlyArg-----ProAspAlaProva 155
Qy 263 GCGTGTACATGCTTCGGCCCTTGTATTGGTCTGCTCCGCCAAACACAGCAAGCTCATGAAC 204
Db 155 lArgArg-----AlaProAlaAsnSerVal----- 163
Qy 203 TTGACCTGCTTCATCTTCTGCTCTTGCAATGTCAGGGACTCGAAGAGGGCAGCAGCTCC 144
Db 164 -ProAlaSerArgGlyArgAlaGlyCysSerArgPheArgCysArgThrProAlaPr 182
Qy 143 GGGTCAGCCAGCACCTTATCTAGAAGGTGTCAACCGCAGCTTCATGCTTCTGCGCCG 84
Db 182 oGlyAlaProAlaArgProAlaGlyArgArgSerProProAlaArgCys-----Ar 199
Qy 83 CCCAGGTTCATCAACAGCTTCTTGGCCCGCATCCGCTTCGCGCG 38
Db 199 gSerGlyCysAlaAlaAlaArgGlyProProValProValProPro 214
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Job time : 33.5 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2006, 10:30:49 ; Search time 20.8 Seconds  
(without alignments)  
3995.228 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1122

Sequence: 1 gcgcgtcgcagacggc.....agccatttttcgaccacgaagcc 598

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-USER=US0920953 @CNC 1 1 342 @runat 10082006 163819 5480 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.Main:

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254.5	22.7	124	4	US-10-282-122A-61519
2	148	13.2	324	4	US-10-425-114-58160
3	148	13.2	428	6	US-11-096-568A-19503
4	148	13.2	544	6	US-11-096-568A-19501
5	142.5	12.7	19723	4	US-10-084-846A-5
6	138.5	12.3	212	6	US-11-096-568A-22256
7	128	11.4	210	6	US-11-096-568A-8162
8	125	11.1	417	4	US-10-437-963-143835
9	125	11.1	19695	4	US-10-084-846A-3
10	124.5	11.1	19662	4	US-10-084-846A-6
11	120.5	10.7	19608	4	US-10-084-846A-8

12	120	10.7	375	6	US-11-096-568A-23618	Sequence 23618, A
13	119.5	10.7	276	4	US-10-437-963-166380	Sequence 166380, A
14	117.5	10.5	309	6	US-11-096-568A-18960	Sequence 18960, A
15	117.5	10.5	384	4	US-10-425-114-72136	Sequence 72136, A
16	117.5	10.5	384	4	US-10-425-114-72137	Sequence 72137, A
17	117.5	10.5	19723	4	US-10-084-846A-5	Sequence 5, Appli
18	117	10.4	325	6	US-11-096-568A-24112	Sequence 24112, A
19	117	10.4	369	6	US-11-096-568A-24111	Sequence 24111, A
20	117	10.4	373	6	US-11-096-568A-24110	Sequence 24110, A
21	116.5	10.4	19652	4	US-10-084-846A-7	Sequence 7, Appli
22	115.5	10.3	155	4	US-10-437-963-103601	Sequence 103601, A
23	115.5	10.3	224	4	US-10-437-963-141171	Sequence 141171, A
24	115.5	10.3	517	4	US-10-425-114-63757	Sequence 63757, A
25	115.5	10.3	517	4	US-10-425-114-63798	Sequence 63798, A
26	115.5	10.3	517	4	US-10-425-114-63800	Sequence 63800, A
27	115.5	10.3	728	4	US-10-425-114-63691	Sequence 63691, A
28	115	10.2	274	4	US-10-425-115-293205	Sequence 293205, A
29	114.5	10.2	381	4	US-10-425-114-47573	Sequence 47573, A
30	114.5	10.2	401	4	US-10-425-114-40384	Sequence 40384, A
31	114.5	10.2	599	5	US-10-450-763-33889	Sequence 33889, A
32	113.5	10.1	398	4	US-11-096-568A-21569	Sequence 21569, A
33	112.5	10.0	352	6	US-11-096-568A-21570	Sequence 21570, A
34	112.5	10.0	355	6	US-11-096-568A-21569	Sequence 21569, A
35	112	10.0	139	6	US-11-096-568A-25691	Sequence 25691, A
36	112	10.0	247	4	US-10-425-114-48205	Sequence 48205, A
37	112	10.0	19725	4	US-10-084-846A-4	Sequence 4, Appli
38	111	9.9	265	4	US-10-437-963-176482	Sequence 176482, A
39	111	9.9	424	6	US-11-096-568A-22088	Sequence 22088, A
40	110.5	9.8	294	4	US-10-437-963-106950	Sequence 106950, A
41	110.5	9.8	464	6	US-11-096-568A-12965	Sequence 12965, A
42	110.5	9.8	492	4	US-10-425-114-65735	Sequence 65735, A
43	110	9.8	249	5	US-10-370-715B-636	Sequence 636, App
44	109.5	9.8	424	6	US-11-096-568A-22088	Sequence 22088, A
45	109.5	9.8	530	4	US-10-425-114-66510	Sequence 66510, A

#### ALIGNMENTS

#### RESULT 1

US-10-282-122A-61519  
; Sequence 61519, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Orlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamanoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR FILING DATE: 2000-11-27

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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61519
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Legionella pneumophila
US-10-282-122A-61519

Alignment Scores:
Pred. No.: 1,01e-15 Length: 124
Score: 254.50 Matches: 49
Percent Similarity: 64.1% Conservative: 26
Best Local Similarity: 41.9% Mismatches: 41
Query Match: 22.7% Indels: 1
DB: 4 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)
QY 61 AAGAGCTGTTGATGACCTGGCGGCCGACAGGATGAGCTGGCGGTTGACACCTTC 120
Db 3 GluSerLeuPheGluArgLeuGlyGlyGlnAsnAlaValAsnThrAlaValAspPhe 22
QY 121 TACGATGAAGGTGCTGGCTGACCGCGGAGTGTGCTGCTTCTTCGAGTCCCTGGACATCAA 180
Db 23 TyrArgLysMetLeuMetAspAspArgValAsnThrPhePheAspValAspMetGlu 42
QY 181 GAGCAGAGATGAAGCAGGTCAAGTTCATGACCTTCGTTGCGGAGCAGACCAATAC 240
Db 43 GlnGlnIleLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
QY 241 AAGGCCGAGCATGTACGACCGCACACCCCATCTGTGTCAAGGCCACGGCTGACAC 300
Db 63 ThrGlyLysSerMetArgGlyGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
QY 301 CGCCACATTTGACAGATCAAGCAGCTACTTGGAGAGAGCGCTGCAAGAGATGGCGTCAAG 360
Db 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101
QY 361 CAGATGTGATCCAGCAGCGCGCGGAGTGTGGAGTCCACCCCGCAGCAA 411
Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2
US-10-425-114-58160
; Sequence 58160, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58160
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI.pep
US-10-425-114-58160
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Alignment Scores:
Pred. No.: 2.95e-05 Length: 324
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)
QY 5 TGCCTGCAGACGGG-----CCACGAGCACCACAGACGCGCGGAACGG 49
Db 84 CysAlaArgThrArgAlaArgThrThrAlaProSerAlaProCysThrArgArgThr 103
QY 50 GATCGGCGCAAGAAGCTGTTTGTGACCTGGCGCGCGCAGAGGATGAAGCTGCGG 109
Db 104 SerSerGlySerArgAlaCys-----CTGACCCGAGCTGCTGC 110
QY 110 TTGACACCTTCTACGATAAGTCTGG-----CTGACCCGAGCTGCTGC 154
Db 111 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 128
QY 155 CCTTCTTCGAGTCCCTGGACATCAAGAGCAGAGAAGATGAAGCAGGTCAAGTTCATGAGCT 214
Db 129 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerArgAla 147
QY 215 TCCTGTTTGGCGGAGCAGACCAATACAAGGCGCGAAGCATGTACGACGACACGCGCCATC 274
Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProG 167
QY 275 TGTG-----CAAGGCCACGGCTGGACACCGCCACTTTTGACAAGATCAAGCAGTACC 328
Db 167 nGlyThrProArgProArgPro---ThrSerArgThrSerSerAlaArgSerSerThr 186
QY 329 TTGACGAGAGCGCTGCAAGAGA-----TGGCGCGTCAAGCAGGATGTGATCC 373
Db 187 -----SerAlaCysThrArgProAlaAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 204
QY 374 AGCACCGCCCGGAGTGTGGAGTCCACCGCGCGAAGATTTGACTTNCACCAACAACTGCG 433
Db 205 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 223
QY 434 CACCAACTGATTTTCATTAAACCAACCCAGCTGAGCGCTCATTCCTCATTTTGAG 493
Db 224 -----ProGlnAlaAlaAlaSerGlyThrSerTrpArg 234
QY 494 -----CGGGAGCGCCAGTTGCCGAGCGCGCCAGGGGCGCCAGGAGCTGCA 541
Db 235 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253
QY 542 AATCGTTTGCAGCCCTTGTGCA 565
Db 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3
US-11-096-568A-19503
; Sequence 19503, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19503
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)..(428)
; OTHER INFORMATION: Ceres Seq. ID no. 12373378
US-11-096-568A-19503

Alignment Scores:
Pred. No.: 3,17e-05 Length: 428
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 6 Gaps: 10

US-09-920-953-2 (1-598) x US-11-096-568A-19503 (1-428)
QY 5 TGCCTGCAGACGGG-----CCACAGCACCACAGACGCGGGAAGCGG 49
Db 221 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 240
QY 50 GATCGGCGCAAGAAGCTGTTTGATGACCTGGCGCGGCGAGGCGATGAAGCTGGCGG 109
Db 241 SerSerGlySerArgAlaCys-----
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGGAGCTGCTGC 154
Db 248 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 265
QY 155 CCTTCTTCGAGTCCCTGCAGATGCAAGACGACAGATGAACAGGTCAAGTTCTAGACT 214
Db 266 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerAla 284
QY 215 TCGTGTGTTGGCGGAGCAGCAATACAGGCGCGGAGCATGTACGACGACACGCCCATC 274
Db 285 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 304
QY 275 TGGT-----CAAGGGCCACGGCTGGACACCCACTTTGACCAAGATCAAGCAGTACC 328
Db 304 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 323
QY 329 TTGAGAGACGCTCAAGAGA-----TGGCGCTCAAGCAGATGTATCC 373
Db 324 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 341
QY 374 AGCAGCGCGCGGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCCTCAACACTGCG 433
Db 342 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 360
QY 434 CACCCAACTGATTTTCATTACCAACCCAGCCCTGAGCGCTCATTCCTCGATTTTCAG 493
Db 361 -----ProGlnAlaAlaSerGlyThrSerTrpArg 371
QY 494 -----CGGGAGCGCCAGTTGCGAGCGCGCCAGGCGGCGCCAGGAGCTGCA 541
Db 372 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 390
QY 542 AATCGTTTGCAGCCCTTGCTGCA 565
Db 391 GlyArgAlaSerSerAlaThrAla 398

RESULT 4
US-11-096-568A-19501
; Sequence 19501, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19501
; LENGTH: 544
; TYPE: PR

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; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 12373376
US-11-096-568A-19501

Alignment Scores:
Pred. No.: 3,37e-05 Length: 544
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 6 Gaps: 10

US-09-920-953-2 (1-598) x US-11-096-568A-19501 (1-544)
QY 5 TGCCTGCAGACGGG-----CCACAGCACCACAGACGCGGGAAGCGG 49
Db 337 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 356
QY 50 GATCGGCGCAAGAAGCTGTTTGATGACCTGGCGCGGCGAGGCGATGAAGCTGGCGG 109
Db 357 SerSerGlySerArgAlaCys-----
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGGAGCTGCTGC 154
Db 364 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 381
QY 155 CCTTCTTCGAGTCCCTGCAGATGCAAGACGACAGATGAACAGGTCAAGTTCTAGACT 214
Db 382 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerAla 400
QY 215 TCGTGTGTTGGCGGAGCAGCAATACAGGCGCGGAGCATGTACGACGACACGCCCATC 274
Db 401 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 420
QY 275 TGGT-----CAAGGGCCACGGCTGGACACCCACTTTGACCAAGATCAAGCAGTACC 328
Db 420 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 439
QY 329 TTGAGAGACGCTCAAGAGA-----TGGCGCTCAAGCAGATGTATCC 373
Db 440 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 457
QY 374 AGCAGCGCGCGGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCCTCAACACTGCG 433
Db 458 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 476
QY 434 CACCCAACTGATTTTCATTACCAACCCAGCCCTGAGCGCTCATTCCTCGATTTTCAG 493
Db 477 -----ProGlnAlaAlaSerGlyThrSerTrpArg 487
QY 494 -----CGGGAGCGCCAGTTGCGAGCGCGCCAGGCGGCGCCAGGAGCTGCA 541
Db 488 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 506
QY 542 AATCGTTTGCAGCCCTTGCTGCA 565
Db 507 GlyArgAlaSerSerAlaThrAla 514

RESULT 5
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MOHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A

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Qy 31 TGGTCTGTGGT 20  
Db 186 TrpSerTrpTrp 189

RESULT 7  
US-11-096-568A-8162  
; Sequence 8162, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096, 568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 8162  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(210)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177853  
US-11-096-568A-8162

Alignment Scores:  
Pred. No.: 0.00232 Length: 210  
Score: 128.00 Matches: 55  
Percent Similarity: 36.9% Conservative: 20  
Best Local Similarity: 27.1% Mismatches: 75  
Query Match: 11.4% Indels: 53  
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-11-096-568A-8162 (1-210)

Qy 530 GGGCCCCCTGGCGCTCGCACTGGCGCTCCCGCTCAAAATCGATGATGAGCGC 471  
Db 13 GlyArgGlyGlnAlaArgSerGluInProTrpLeuArgArgTrpProArg 32  
Qy 470 -----TCAGGCTGGGGTTGG---GTTAATGAAATCACTGGTGGCGCAGTTG 426  
Db 33 ArgAlaArgSerSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 52  
Qy 425 TTGGGNAAG----- 417  
Db 53 ArgGlySerAlaSerAlaArgArgProArgArgArgProArgProArgPro 72  
Qy 416 -----TCAATTCGTGGCGGTGGACTCCACCACTCCGCGCGCTGC 375  
Db 73 ProThrGlyArgCysGlySerProAlaArgArgProSerThrSerThrGlyArgSer 92  
Qy 374 TGGATCATCTGCTTCACGCCCATCTCTTCAGCGCTCTCCAAAGTACTGCTTGATC 315  
Db 93 SerAlaThrAlaSerThrPro---SerAlaLeuGlySerProArgSerThrCysSer 111  
Qy 314 TTGTCAAAGTGGCGTGTTCAGGCGGTGGCCCTTGACCAAGTGGCGTGTGCGTGTAC 255  
Db 112 ThrThrTrpTrpProTrpThrArgThrTrpProArgThr---TrpArgAlaArgSer--- 129  
Qy 254 ATGCTTGGCCCTGTATGTGTCTCTCCG-----CCAAACAGAAAGTCTATG 207  
Db 130 -----SerAlaProGlySerArgThrProTrpSerSerProPro 142  
Qy 206 AACTTGACCTGCTTCATCTTCTGCTCTGATGTCCAGGACTCGAAGAGGCGAGCAGC 147  
Db 143 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 157  
Qy 146 TCCGGGTGAGGCGAGCAGCTTATCTAGAGAGTGTCAACCGCAGCTTCTCTCTCGC 87  
Db 158 SerAlaSerSerThrValAla-GlyProCysSerProProSerAla----- 173  
Qy 86 CCGCCAGGTATCAAAACAGCTTCTTGGCGCGGATCCCGCTTCCGCGCTCTCTGTGGTG 27

Db 174 ----ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 192  
Qy 26 CTGGTGG 20  
Db 192 rTrpTrp 194

RESULT 8  
US-10-437-963-143835  
; Sequence 143835, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 143835  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_44705C.1.pep  
US-10-437-963-143835

Alignment Scores:  
Pred. No.: 0.00543 Length: 417  
Score: 125.00 Matches: 63  
Percent Similarity: 36.2% Conservative: 13  
Best Local Similarity: 30.0% Mismatches: 74  
Query Match: 11.1% Indels: 60  
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

Qy 23 CCAGCACACAGACGCGGAGCGGATGCGGCGCAAGAAAGTGTGTGATGACCTGG 82  
Db 22 ProThrProHisArgArgGlu-----IleGluArgTrp 32  
Qy 83 GCGCGCAGAGGATGAGCTGGCGGTGACACTTCTAGCATAAGTGTGGTGGTACC 142  
Db 33 Leu-----ProTrpArgSerAlaProPro-----ThrThr 43  
Qy 143 CGGAGCTGCTGC-----CCTTCTTCGAGTCCCTCGACATGCAAGAGCAGA 187  
Db 44 GlySerCysSerThrProThrThrProProProProProProProProProPro 62  
Qy 188 AGATGAAGCAGGTCACAGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAGGGCC 247  
Db 63 -----SerArgSerLeuProAlaThrProProProAlaProThrLysArgArg--- 79  
Qy 248 GAAGCATGTACGACGACACGCCCATCTGTCAAGGCGCAGGCTGGACCAACCGCCACT 307  
Db 80 -----ArgThrThrArgTrp---GlyAlaThr 87  
Qy 308 TTGCAAGATCAACAGCTACTCTGGAG-----AGACGTGCAAG 346  
Db 88 LeuThrAlaThrThrSerThrAlaGluAsnSerArgArgArgThrArgArgAlaArgArg 107  
Qy 347 AGATGGGCGTCAAGCAGGATGTGATCCAGCAGCGCGCGGAGTGTGTGAGTCCA----- 400  
Db 108 ArgArgGlyArgSerArgAlaSerSerThrThrProProProProProProProPro 127  
Qy 401 ---CCCGCAGGAATTTGACTTTCCTCCCAACAACTGCGCACCACTGATTTTCAATAACC 457

```
Db 128 SerProSerThrProSerAlaAlaProSerThrSerSerProThrArgAlaSerProPro 147
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 458 AACCCCGCTGAGCGCTCATTCATCGATTTGAGCGGGGAGCGCCAGTTCCCGAGCGC 517
||||:||||| |||:||||: |||:||||| |||:|||||
Db 148 TyrArgSerThrSerProSerSerProPro--ProAlaAlaSerSerAlaAlaAla 167
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 518 GCCCAGGGGGCCCA-----GGAGCCTGCAAACTCGTTTG 550
||||:||||| |||:||||: |||:||||| |||:|||||
Db 167 rGProProAlaProThrThrSerProThrArgProProSerGlyGlyCysAlaSerLeuA 187
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 551 CCAGCCCTTGCTGCATTGAAGAGCCA 576
||||:||||| |||:||||: |||:||||| |||:|||||
Db 187 laThrProAlaThrThrSerThrPro 195
||||:||||| |||:||||: |||:||||| |||:|||||

RESULT 9
US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.: 0.0147 Length: 19695
Score: 125.00 Matches: 57
Percent Similarity: 35.3% Conservative: 15
Best Local Similarity: 27.9% Mismatches: 68
Query Match: 11.1% Indels: 64
DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)
Qy 2 CGTCTCGTCGAGAGC---CGGCCACGACGACGCGGAGCGGATGCGGGC 58
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgSerArgSerProAla 11343
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 59 GCAAGA-----AGCTGTTGTATGACCTGGCGCGGCGAGAGCATGAAGC 103
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11344 AlaArgThrTrpArgCysGlyAlaAlaSerThrThrTrpAlaAlaGlyArgArg----- 11361
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 104 TGGCGGTGACACCTTCTACATAAGG-----TGCTGG----- 136
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11362 -----SerAlaValArgLysAsnCysTrpSerSerSerThrProArgPro 11376
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 137 -----CTGACCGGAGCTGCTCCCTTCTTCGAGTCCCTCGACATGC 178
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpPro 11396
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 179 AAGAGCAGAGATGAAGCAGTCAAGTTCA-----TGAGCTTCGTGTTG 223
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11397 AspSerSerProCysProArgCysSerSerTrpThrProProAlaSerThrArg 11416
||||:||||| |||:||||: |||:||||| |||:|||||

Qy 224 GCGAGCAGAGCC-----AATCAAGGGCGCGAAGCATGT 256
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerArgAlaProProCys 11436
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 257 ACAGCAGCACAGCCCATCTGTCGTCGAGGCGCACGCGCTGGACCCGCTTTTGACAAGA 316
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11437 CysSerProArgSerThrTrpArgArg-----ProThrGlySerProThrArg 11452
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 317 TCAAGCAGTACCTTGGAGAGACGCTCGAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 377 ACGCCGCGGAGTGTGGAGT-----CCACCGCGGAGC--- 409
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11467 ArgProSerProTrpTrpAlaAlaThrGlySerTrpTrpArgProProArgThrCys 11486
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 410 -----AATTTGACTTNCCTCAACAACTGCGCACCCAACTGATTTTCAATTAACCCCAAC 460
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11487 ArgProProArgLeuArgSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 461 CCCAGCCTGAGC 472
||||:||||| |||:||||: |||:||||| |||:|||||
Db 11507 ProAlaValSer 11510
||||:||||| |||:||||: |||:||||| |||:|||||

RESULT 10
US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-6

Alignment Scores:
Pred. No.: 0.0165 Length: 19662
Score: 124.50 Matches: 56
Percent Similarity: 33.0% Conservative: 14
Best Local Similarity: 26.4% Mismatches: 64
Query Match: 11.1% Indels: 78
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)
Qy 536 GTCCTGGCGCCCTGGGCGCGCTCGGCAACTGGCG---CTCCCCGCTCAAAATCGATGG 480
||||:||||| |||:||||: |||:||||| |||:|||||
Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 479 AATGACCGCTCAGGCTGGGTTGGTTAATGAAATCAGTTGGTGCGGAGTTGTTGGN 420
||||:||||| |||:||||: |||:||||| |||:|||||
Db 19348 -----ProGlyProGlyTrp----- 19352
||||:||||| |||:||||: |||:||||| |||:|||||
Qy 419 AAGTCAATTCGTGGCGGTGGACTCCACCACTCCGCGCGGCTGGATCATCATCC--- 363
||||:||||| |||:||||: |||:||||| |||:|||||
Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368
||||:||||| |||:||||: |||:||||| |||:|||||
```

```
QY 362 -----TGCTTGAGCCCATCTCTTCGAGGGTCTCTCCA 330
Db 19369 ArgCysSerGlyArgSerArgCysThrAlaCysCysSerProCysAlaSer 19388
QY 329 AGGTACTGC---TTGATCTTGTCAAAGTGGCGG-----TGGTCAGG----- 291
Db 19389 ArgArgCysGlyCysAlaGlyAlaThrTyrArgProArgArgTyrTyrArgSerPro 19408
QY 290 ---CCGTGGCCCTTGACAGATGGCGGTGCGTCGTACATGCTTCGGCCCTTGATGG 234
Db 19409 SerProTyrGlyTyrCysArgTyrProThrAlaAlaGlyGlySerAlaAspThrTyrGly 19428
QY 233 TCTGCTCGCCCAACACG----- 216
Db 19429 SerSerProSerProProArgProGlyGlyCysThrGluGlyArgSerProValSer 19448
QY 215 -----AAGCTCATGAACCTTCACCTGCTTCATCTCTCTCTCTGTCATGTCAGG 168
Db 19449 SerProHisGlyArg-SerGlyCysTyrProAlaGlyProArgProAlaAlaGlyProGly 19468
QY 167 GACTCGAAGAGGCACAGCTCCGGTCCAGCCAGCCACCTTATCGTAGAAGGTGTCAACC 108
Db 19468 YAspArgArgGlnAlaLeuSerSerGlySerPro----- 19479
QY 107 GCAGCTTCATGCTCTGCGCCGCCAGGTGCATCAACACAGCTTCTTGGCCGCCATCCC 48
Db 19480 -----ArgArgGlyAlaProSerPheSerAlaAlaArgGlyAl 19493
QY 47 GCTTCCG-----CCGTCTCTGTGCTGCTGGTG 20
Db 19493 aaAlaProThrIleProAlaLeuPheCysSerTyr 19504

RESULT 11
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

Alignment Scores:
Pred. No.: 0.0403 Length: 19608
Score: 120.50 Matches: 49
Percent Similarity: 35.7% Conservative: 16
Best Local Similarity: 26.9% Mismatches: 92
Query Match: 10.7% Indels: 25
DB: 4 Gaps: 7

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)
QY 20 CCACGACACACAGACGCGGAGCGGGATGCGGGCGGACAGACCTGTTTGATGACC 79
::: |||||
```

```
Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438
QY 80 TGGCGCGCAGAGCATGAAGCTGCGGTGACACCTTCTACGATAAGTGTCTGGCTG 139
Db 5439 -----ProProAlaSerThrTyrPro-----SerThrAlaAlaCysTyrPro 5452
QY 140 ACCCGGAGCTGCTGCGCTTCTTCGAGTCCCTGAGATGCAAGAGCAGAGATCAAGCAGG 199
Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgArgProGlyArg 5470
QY 200 TCAAGTTTACGACTTCGTGTTTG---GCGGAGCAGACCAATACAAAGGCCGCGGAGCATGT 256
Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTyrCysProAlaCys 5490
QY 257 ACAGCCACACGCCCATCTGTCAGGCGCACCGCTTGACACCGCCACTTTTGACAAGA 316
Db 5491 ThrSerAsnArgProAlaArgProProThrSerSerTyrProThrArgProArgSerAla 5510
QY 317 TCAAGCAGTACCTTGGAGAGAGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376
Db 5511 ProArgProSerThrSerArgSerThrAlaArgTyrProSerProAsnTyrSerArgAsp 5530
QY 377 AGCGCCCGGAGTGTGGAGTCCACCCGCGACGAATTTGACTTNNCCCAACA-----ACT 430
Db 5531 TtrProThrSerThrThrProSerProAlaAlaGThrArgThrAlaProSerArgArgThr 5550
QY 431 GCGCACCCCACTGATTTTTCATTAACCAACCCAGCTGAGCGCTCATTCATCGATGTTT 490
Db 5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567
QY 491 GAGCGGGGAGCGCAGTTCGCGAGCGGCCCGCCAGGGGGCCAGGAGCTGCAAAATCGTTG 550
Db 5568 ArgProArgThrProValTyrArgArgProGlyCysProHisArgSerAlaArgLeu 5587
QY 551 CCAGCC 556
Db 5588 ProAla 5589

RESULT 12
US-11-096-568A-23618
; Sequence 23618, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23618
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(375)
; OTHER INFORMATION: Ceres Seq. ID no. 12414168
US-11-096-568A-23618

Alignment Scores:
Pred. No.: 0.0162 Length: 375
Score: 120.00 Matches: 56
Percent Similarity: 37.2% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 92
Query Match: 10.7% Indels: 38
DB: 6 Gaps: 8

US-09-920-953-2 (1-598) x US-11-096-568A-23618 (1-375)
QY 5 TGCTGCGAGCGGGCCACCCAGCAGCAGCAGCGGAGCGGGATGCGGGCGCAAGA 64
Db 172 CysArgAlaThrArgProAlaAlaProSerArgThrThrSerProCysAla----- 188
```



```
QY 65 AGCTGTTGATGACCTGGCGGCGCCAGAGCATGAAGCTGGCGGTTGACACCTTCTACG 124
Db 189 -----SerValAlaArgProArgThrTrpProProSerPro----- 200
QY 125 ATAAGGTGCTGGCTGACCGGAGCTGCGCTTCTTCGAGTCCCTGGACATGCAAGAGC 184
Db 201 -----CysGlyAspThrSerSerCysHisSerSerAlaAlaThrProAlaArgGly 218
QY 185 AGAAGATGAAGCAGGTCAAGTTCAATGAGCTTCGTTTGGCGGAGCAGACCAATACAAG 244
Db 219 ArgArgProSerAlaProProThrLeuSerSerThrGlyProSerThrAlaThrGly 238
QY 245 GCCGAGCATGTACGACGCGACACGCCCATCTGGTCAAGGCGCCAGGCTGGACACCGCC 304
Db 239 AlaCysArgCys-----ArgArgAlaProArgProThrThrPro 251
QY 305 ACTTTGACAAGATCAAGCAGTACCTTGGAGAGAGCTGCAAGAGTGGCGGTCAAGCAGG 364
Db 252 TrpProThrArgSerAlaProAlaArg-----ArgArgTrpThrProSer--- 266
QY 365 ATGTGATCCAGCAGCGCGCGAGTGGTGGAGTCCACCCCG-----ACGAATTG 415
Db 267 -----SerSerArgProPro-----TrpSerSerAlaAlaThrSerSerThr 282
QY 416 ACTTNCACAACACTGGCGACCCCACTGATTTTCATTAACCCACCCAGCCTGAGGCT 475
Db 283 ThrAlaProSerThrThrProProGlySerGlyProProGlySerProSerTrpSerGly 302
QY 476 CATTTCATCATGATTGAGCGGGAGCG-----CCAGTTGCGGAGCGC 517
Db 303 ThrSerThrAlaSerSerThrAlaSerSerProSerThrProGlyProThrProPro 322
QY 518 GCCAGGGGCGCCAGGAGCTGCAATCGTTTGCAGCCCTTCTGTCGATTGAAGAGCCAT 577
Db 323 SerSerCysAlaSerSerSerAlaSerSerThrProThrAlaAlaSerThrSerThr 342
QY 578 CAGCCATTTCGCACCAAGCC 598
Db 343 ThrSerValSerAsnSerSer 349

RESULT 13
US-10-437-963-166380
; Sequence 166380, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166380
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(276)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65095C.1.pap
US-10-437-963-166380

Alignment Scores:
Pred. No.: 0.027 Length: 309
```

```
Pred. No.: 0.0167 Length: 276
Score: 119.50 Matches: 52
Percent Similarity: 35.1% Conservative: 15
Best Local Similarity: 27.2% Mismatches: 69
Query Match: 10.7% Indels: 55
DB: 4 Gaps: 8

US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)

QY 29 CCACAGAGCGCGGAGCGGATGCGGCGCAAGAGCTGTTTGATGACCTGGCGGCGG 88
Db 3 ProArgArgArgArgArgArgileCysThrValArg----- 14
QY 89 CAGAAGCATGAAGCTGGCGGTTGACACCTTCTACAGTAAGGTGCTGGTGCACCCGAGC 148
Db 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25
QY 149 TGCTGCTCTTTCGAGTCCCTGGAGATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCA 208
Db 26 AlaSerProSerSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCGCGAGCATGTACGAGC----- 262
Db 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACAGCCCATCTGTTCAAGGCGCCAGGCTTGACCCACCGCCACTTTGACAAAGATCA 319
Db 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79
QY 320 AGCAGTACCTTGGAGAGCGCTGC-----AAGAGATGGCGCTCAAGCAGGAGTGCA 370
Db 80 ArgSerGlySerCysArgGlyCysCysPheArgArgTrpArgSerThrArg----- 97
QY 371 TCCAGCAGCGCGCGGAGTGGTGGAGTCCACCGCGCAGCAATTGACTTNCACCAACT 430
Db 98 -----ProAlaAlaProSerSerAlaSerProThrGly 108
QY 431 GGCACCCCAACTGATTTCATTAAACCCACCCAGCCTGAGCGCTCATTCATCGATTTT 490
Db 109 AlaSerThrThrSer-----ProSerProThr----- 117
QY 491 GAGCGGGAGCGCCAGTTCGCGAGCGCGCCAGGCGCCAGGAGCTCTCAATCGTTTG 550
Db 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAspGlySer***Cys 133
QY 551 CCAGCCCTTGTGCTGATTGAAGAGCCATCAGCCA 583
Db 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

RESULT 14
US-11-096-568A-18960
; Sequence 18960, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18960
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(309)
; OTHER INFORMATION: Ceres Seq. ID no. 12367975
US-11-096-568A-18960

Alignment Scores:
Pred. No.: 0.027 Length: 309
```

Score: 117.50 Matches: 75  
Percent Similarity: 36.7% Conservatives: 15  
Best Local Similarity: 30.6% Mismatches: 86  
Query Match: 10.5% Indels: 69  
DB: 6 Gaps: 13

US-09-920-953-2 (1-598) x US-11-096-568A-18960 (1-309)

```
QY 15 CGCGGCCACACAGC-----CACAGAGCGCGGAGCGGATGCGGCGCGCAAGAAGCT 68
DB 57 ArgGlyHisArgHisProSerHisArgProLeuAlaSerValArgGln-----72
QY 69 GTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGCG-----107
DB 73 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyArgGlyGlu 87
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
DB 88 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspHisGlyAla 107
QY 135 GCGTGACCGGAGCTGCTGCTTTCGAGTCCCTGGACATGCA-----AGAGCA 185
DB 108 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 127
QY 186 GAAGATCAACAGCAGTCAAGTTCATGAGCTTCGTGTTTGGCGGACAGCA-----236
DB 128 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 147
QY 237 ATCAAGGGCGGAGCATGTACGACGACACGCGCCATCTGCTCAAGGGCGCGCTGGA 296
DB 148 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlyCysArgGlyArg 167
QY 297 CCACCGCCACTTTGACAAGATCAAGCAGTACCT-----TGAGAGAGCGCT 341
DB 168 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeuGlnArgGlyAla 187
QY 342 GCA-----AGAGATGGCGT-----CAACGAGATGTGATCCAGCA 377
DB 188 GlyGlyValArgGlnSerAspGlyArgAlaGlyValGlnAlaAlaGlyAlaAsp--ArgS 207
QY 378 CGCGCGCGGAGTGGTGAGTCCACCGCGCAGCAAT---TTGACTTNCACCAACATCGCG 434
DB 207 erGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProAspLeuH 227
QY 435 ACCCACTGATTTTCATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGAGC 494
DB 227 isProAlaGlu-----ProLeuProSerLeuProGluProArgProGlyProArg 244
QY 495 GCGGAGCG-----CCAGTTGCGGCGCGCGCGCGGGG 527
DB 244 rgGlyAlaAlaGlnGlyArgArgProAspHisProValProGlyArgArgArgGlyA 264
QY 528 CCAGGAGCGCTGCA-----AATCGTTTCCAGCCCTTGTGCTATTGA 569
DB 264 laArgArgProAlaAlaLeuArgArgValGlyProArgGlnAlaArgAlaArgLeuV 284
QY 570 AGAGCCATCAG 580
DB 284 alHisGln 287
```

## RESULT 15

US-10-425-114-72136  
; Sequence 72136, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 72136  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3245-558-Al\_FLI.pep  
US-10-425-114-72136

Alignment Scores:  
Pred. No.: 0.0285 Length: 384  
Score: 117.50 Matches: 69  
Percent Similarity: 37.9% Conservatives: 16  
Best Local Similarity: 30.8% Mismatches: 74  
Query Match: 10.5% Indels: 65  
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

```
QY 15 CGCGGCCACACAGC-----CACAGAGCGCGGAGCGGATGCGGCGCGCAAGAAGCT 68
DB 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln-----69
QY 69 GTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGCG-----107
DB 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
DB 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspArgGlyAla 104
QY 135 GCGTGACCGGAGCTGCTGCTTTCGAGTCCCTGGACATGCA-----AGAGCA 185
DB 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 124
QY 186 GAAGATCAACAGCAGTCAAGTTCATGAGCTTCGTGTTTGGCGGAGCAGCAATACAGGG 245
DB 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGCGCACCGCCATCTGCTCAAGGGCCA 287
DB 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACACCGCGCACTTTGACAGATCAA 320
DB 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGAGACCTCGAAGATGCGCGT-----CAAGCAGGATGT 368
DB 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGGTGAGTCCACCGCGCAGCAAT---TTGACTTNCCTCAA 425
DB 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221
QY 426 CAACTGCGCACCCCACTGATTTTCATTAAACCCAGCTGAGCGCTCATTCCTCATCG 485
DB 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu-----234
QY 486 ATTTGAGCGGAGCGCGCGAGCTGTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
DB 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgArgProAspHisP 253
QY 546 GTTTGCCA 553
DB 253 roValPro 255
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Search completed: August 11, 2006, 10:35:52  
Job time : 147 secs



GenCore version 5.1.9  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2006, 10:31:55 ; Search time 3.6 Seconds  
(without alignments)  
3354.382 Million cell updates/sec

Title: US-09-920-953-2  
Perfect score: 1122  
Sequence: 1 gcgtgctgcagacgggc.....agccatttttcacacaagcc 598

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 479828

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/abs/ABSSWEB.spool/US0920953/runat 10082006.163820.5518/app query.fasta\_1  
-DB=Published Applications AA New -QFMT=fastan -SURFIX=rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pcr -THR MAX=100  
-MAXLEN=2000000000 -HOST=abs02p  
-USR=US0920953.qcgn 1.1.46 @runat 10082006.163820.5518 -NCPU=6 -ICPU=3  
-NO MAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB.pcp:  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pcp:  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pcp:  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pcp:  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pcp:  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pcp:  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pcp:  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	13.2	428	7	US-11-056-355B-2964
2	148	13.2	544	7	US-11-056-355B-2962
3	138.5	12.3	212	7	US-11-056-355B-7635
4	136	12.1	214	6	US-10-953-349-30500
5	128	11.4	210	7	US-11-056-355B-51768
6	123.5	11.0	358	6	US-10-953-349-28428
7	120	10.7	375	7	US-11-056-355B-3621
8	117.5	10.5	309	7	US-11-056-355B-3480
9	117	10.4	325	7	US-11-056-355B-18635
1	148	13.2	428	7	US-11-056-355B-18634
2	148	13.2	544	7	US-11-056-355B-2962
3	138.5	12.3	212	7	US-11-056-355B-7635
4	136	12.1	214	6	US-10-953-349-30500
5	128	11.4	210	7	US-11-056-355B-51768
6	123.5	11.0	358	6	US-10-953-349-28428
7	120	10.7	375	7	US-11-056-355B-3621
8	117.5	10.5	309	7	US-11-056-355B-3480
9	117	10.4	325	7	US-11-056-355B-18635

## ALIGNMENTS

RESULT 1  
US-11-056-355B-2964  
; Sequence 2964, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 2964  
; LENGTH: 428  
; TYPE: prt  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(428)  
; OTHER INFORMATION: Ceres Seq. ID no. 12373378  
US-11-056-355B-2964

Alignment Scores:  
Pred. No.: 4.06e-06 Length: 428  
Score: 148.00 Matches: 62  
Percent Similarity: 38.1% Conservative: 18  
Best Local Similarity: 29.5% Mismatches: 77  
Query Match: 13.2% Indels: 53  
DB: 7 Gaps: 10

Sequence 18634, A  
Sequence 18633, A  
Sequence 40564, A  
Sequence 16356, A  
Sequence 16355, A  
Sequence 33290, A  
Sequence 3578, Ap  
Sequence 25350, A  
Sequence 8234, Ap  
Sequence 16007, A  
Sequence 45786, A  
Sequence 32673, A  
Sequence 68075, A  
Sequence 16007, A  
Sequence 3800, Ap  
Sequence 30498, A  
Sequence 51766, A  
Sequence 5415, Ap  
Sequence 46957, A  
Sequence 18087, A  
Sequence 25756, A  
Sequence 16395, A  
Sequence 5230, Ap  
Sequence 9888, Ap  
Sequence 16356, A  
Sequence 16355, A  
Sequence 39304, A  
Sequence 3637, Ap  
Sequence 41551, A  
Sequence 6754, Ap  
Sequence 16279, A  
Sequence 65494, A  
Sequence 48083, A  
Sequence 26990, A  
Sequence 32400, A  
Sequence 53792, A

US-09-920-953-2 (1-598) x US-11-056-355B-2962 (1-428)

Score: 148.00 Matches: 62  
Percent Similarity: 38.1% Conservative: 18  
Best Local Similarity: 29.5% Mismatches: 77  
Query Match: 13.2% Indels: 53  
DB: 7 Gaps: 10

US-09-920-953-2 (1-598) x US-11-056-355B-2962 (1-544)

Qy 5 TGCTTCAGACGGG-----CCACGACCAACAGAGACGGCGGAGCGG 49  
Db 337 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 356  
Qy 50 GATCGGGCGCAGAGAGCTGTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGGCGG 109  
Db 357 SerSerGlySerArgAlaCys-----CTGACCCGAGCTGCTGC 154  
Qy 110 TTGACACCTTCTACGATAAGTGTCTGG-----CTGACCCGAGCTGCTGC 154  
Db 364 -----ProSerAlaAlaThrCysTyrPArgTyrAlaAlaThrArgSerArgProThrSer 381  
Qy 155 CTTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCT 214  
Db 382 ProArgTyrPArgProThrCysCysProSerProSer---SerCysSerSerArgAla 400  
Qy 215 TCCTGTTTGGCGGAGCAGACCAATACAGGGCGGAGCATGTACAGCAGCAGCCCATC 274  
Db 401 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProgl 420  
Qy 275 TGGT-----CAAGGGCCACGGCTGGACACCGCCACCTTTCACAGATCAACAGCAGTACC 328  
Db 420 nGlyThrProArgProProArgPro---ThrSerArgThrSerSerAlaArgSerThr 439  
Qy 329 TTGGAGAGACGCTGCAAGAGA-----TGGGCGCTCAAGCAGGATGTGATCC 373  
Db 440 -----SerAlaCysThrArgProAlaAlaThrCysTyrSerThrCysArgAlaThrTrp 457  
Qy 374 AGCACCCCGCGGAGTGTGGAGTCCACCCGCGAGCATTTGACTTNCACCAACTGCG 433  
Db 458 AlaCysAlaThrProThrTyrPArgProProAlaProArgCysThrAlaSerAlaThr 476  
Qy 434 CACCCAACTGATTTTCATTAAACCAACCCAGCCCTGAGCGCTCATTTCCATCATTTTGAG 493  
Db 477 -----ProGlnAlaAlaSerGlyThrSerTyrArg 487  
Qy 494 -----CGGGAGCGCCAGTGTCCGAGCGCGCCAGGGGGCCAGGAGCTGCA 541  
Db 488 ThrTyrArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 506  
Qy 542 AATCGTTTCCAGCCCTTCTGCA 565  
Db 507 GlyArgAlaSerSerAlaThrAla 514

RESULT 3

US-11-056-355B-7635  
; Sequence 7635, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 7635  
; LENGTH: 212  
; TYPE: prt  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(544)  
; OTHER INFORMATION: Ceres Seq. ID no. 12373376

US-11-056-355B-2962

Qy 5 TGCTTCAGACGGG-----CCACGACCAACAGAGACGGCGGAGCGG 49  
Db 221 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 240  
Qy 50 GATCGGGCGCAGAGAGCTGTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGGCGG 109  
Db 241 SerSerGlySerArgAlaCys-----CTGACCCGAGCTGCTGC 154  
Qy 110 TTGACACCTTCTACGATAAGTGTCTGG-----CTGACCCGAGCTGCTGC 154  
Db 248 -----ProSerAlaAlaThrCysTyrPArgTyrAlaAlaThrArgSerArgProThrSer 265  
Qy 155 CTTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCT 214  
Db 266 ProArgTyrPArgProThrCysCysProSerProSer---SerCysSerSerArgAla 284  
Qy 215 TCCTGTTTGGCGGAGCAGACCAATACAGGGCGGAGCATGTACAGCAGCAGCCCATC 274  
Db 285 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProgl 304  
Qy 275 TGGT-----CAAGGGCCACGGCTGGACACCGCCACCTTTCACAGATCAACAGCAGTACC 328  
Db 304 nGlyThrProArgProProArgPro---ThrSerArgThrSerSerAlaArgSerThr 323  
Qy 329 TTGGAGAGACGCTGCAAGAGA-----TGGGCGCTCAAGCAGGATGTGATCC 373  
Db 324 -----SerAlaCysThrArgProAlaAlaThrCysTyrSerThrCysArgAlaThrTrp 341  
Qy 374 AGCACCCCGCGGAGTGTGGAGTCCACCCGCGAGCATTTGACTTNCACCAACTGCG 433  
Db 342 AlaCysAlaThrProThrTyrPArgProProAlaProArgCysThrAlaSerAlaThr 360  
Qy 434 CACCCAACTGATTTTCATTAAACCAACCCAGCCCTGAGCGCTCATTTCCATCATTTTGAG 493  
Db 361 -----ProGlnAlaAlaSerGlyThrSerTyrArg 371  
Qy 494 -----CGGGAGCGCCAGTGTCCGAGCGCGCCAGGGGGCCAGGAGCTGCA 541  
Db 372 ThrTyrArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 390  
Qy 542 AATCGTTTCCAGCCCTTCTGCA 565  
Db 391 GlyArgAlaSerSerAlaThrAla 398

RESULT 2

US-11-056-355B-2962

; Sequence 2962, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 2962  
; LENGTH: 544  
; TYPE: prt  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(544)  
; OTHER INFORMATION: Ceres Seq. ID no. 12373376

US-11-056-355B-2962

Alignment Scores: 4.28e-06 Length: 544  
red. No.:

LOCATION: (1)-(212)  
OTHER INFORMATION: Ceres Seq. ID no. 12408188  
US-11-056-355B-7635

Alignment Scores:  
Pred. No.: 2,9e-05 Length: 212  
Score: 138.50 Matches: 68  
Percent Similarity: 39.8% Conservative: 14  
Best Local Similarity: 33.0% Mismatches: 74  
Query Match: 12.3% Indels: 51  
DB: 7 Gaps: 12

US-09-920-953-2 (1-598) x US-11-056-355B-7635 (1-212)

```
QY 576 TGGCTCTTCAATGACGAGGCTGGCAACAGATTGTCAGGCTCTGGGCCCC---TGG 520
DB 16 TrpLeuHis-----ArgTrpProProArgAlaHisSerTrpAlaProAlaTrp 32
QY 519 -----GGCGCTCGGCAACTGGCGTCCCGCTCCAAATCGATGGAATGAGCGCTCAGG 466
DB 33 ArgThrArgArgHisArgThrGlyAla-----Ser-Trp---ProGlySerGI 47
QY 465 CTGGGTTGGTTAATAAATCAGTTGGTGGCGCAGTTGTTGGGNAAGTCAAAATTCGTC 406
DB 47 ySerGlyTrpAlaAlaArgArgSerLeu-LeuArgArgArgTrp-----A 62
QY 405 GCGGTGGACTCCACACTCCGGCGGCGTGGATACATCTGCTTGAOCGCCATC-- 348
DB 62 rArgHisArgProProLeuThrGlyArgCysGlySerProAlaProTrpArgProThrT 82
QY 347 -----TCTTCAGCGCTCTCCAA 329
DB 82 hrTrpThrAlaArgTrpSerAlaThrThrGlySerThrArgSerValSerGlySerPro- 101
QY 328 GGTACTGCTTGATCTTCAAGTGG---CGGTGGTCCAGGCGGTGGCCCTTGACACAGAT 272
DB 102 --TrpSerThrCysSerSerTrpThrArgTrpThrArgThrTrpProArgMetArgP 121
QY 271 GGGCTGTGCGTGCATACATGCTTCGGCCCTCTGTATGTTGCTCTCGCCAAACAGCAAGC 212
DB 121 roAlaAlaSerSer-----AlaProGlySerSerProProLysSerSerP 136
QY 211 TCATGAACCTGACCTTCATCTTCTGCTTGTGATGTCAGGAGACTCGAAGAGGCA 152
DB 136 roProArgCysSerProThrAlaArgCysSerAlaSerSer-----GlyS 151
QY 151 GCAGCTCCGGGTGACGACACCTTATCGTAGAAGTGTCAACCGCCAGCTTCATGCGCTT 92
DB 151 arAlaSerAlaSerSerSerThrAlaAla-GlyProCysSerProProSerAla----- 168
QY 91 CTGCGCCGCCAGGTATCAAAACAGCTTCTTGGCCCGCATCCCGCTTCGCGCTCTCTG 32
DB 169 -----ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArg 185
QY 31 TGGTCTGGTGG 20
DB 186 TrpSerTrpTrp 189
```

RESULT 4  
US-10-953-349-30500  
Sequence 30500, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 30500  
LENGTH: 214

TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-953-349-30500

Alignment Scores:  
Pred. No.: 5,09e-05 Length: 214  
Score: 136.00 Matches: 57  
Percent Similarity: 37.4% Conservative: 19  
Best Local Similarity: 28.1% Mismatches: 74  
Query Match: 12.1% Indels: 53  
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-10-953-349-30500 (1-214)

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QY 530 GGGCCCCCTGGCGCGCTGGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAGCGC 471
DB 17 GlyArgGlyGlyGlnAlaArgArgSerGluGlnProTrpLeuArgArgTrpProArg 36
QY 470 -----TCAGGCTGGGTTGG---GTTAATGAAATCAGTTGGTGGCGCAGTTG 426
DB 37 ArgAlaArgSerSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 56
QY 425 TTGGGNAG----- 417
DB 57 ArgGlySerAlaSerAlaArgArgProArgArgArgArgProArgArgProArgPro 76
QY 416 -----TCAAAATTCGTCGGCGGTGGACTCCACACTCCGCGCGCGTGC 375
DB 77 ProThrGlyArgCysGlySerProAlaArgArgArgProSerThrSerThrAlaArgSer 96
QY 374 TGGATCACATCTGTCAGCCCATCTCTTGCAGCGTCTCTCCAAGGTACTGCTTGATC 315
DB 97 SerAlaThrThrAlaSerThrPro---SerAlaSerGlySerProArgSerThrCysSer 115
QY 314 TTGCAAAAGTGGCGTGTGCAGGCGGTGGCCCTTGACCAGATGGCGGTGTCGCTGTAC 255
DB 116 ThrThrTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 133
QY 254 ATGCTTCGGCCCTTGTATGTTGCTGCTGCTCCG-----CCAAACACGAAAGTCTATG 207
DB 134 -----SerAlaProGlySerArgThrProThrSerSerProPro 146
QY 206 AACTTGACCTGCTTCATCTTCTGCTTGTGATGTCAGGAGACTCGAAGAGGCGACGAC 147
DB 147 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 161
QY 146 TCCGGGTGACGACGACCTTATCGTAGAAGTGTCAACCGCCAGCTTCATGCTTCTGCG 87
DB 162 SerAlaSerSerSerThrAlaAla-GlyProCysSerProProSerAla----- 177
QY 86 CCGCCCGAGGTATCAAAACAGCTTCTTGGCCCGCATCCCGCTTCGCGCTCTCTGTG 27
DB 178 ---ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 196
QY 26 CTGGTGG 20
DB 196 rTrpTrp 198
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RESULT 5  
US-11-056-355B-51768  
Sequence 51768, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nikolai  
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 51768  
; LENGTH: 210  
; TYPE: prt  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(210)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177853  
US-11-056-355B-51768

## Alignment Scores:

Pred. No.: 0.000304 Length: 210  
Score: 128.00 Matches: 55  
Percent Similarity: 36.9% Conservative: 20  
Best Local Similarity: 27.1% Mismatches: 75  
Query Match: 11.4% Indels: 53  
DB: 7 Gaps: 9

US-09-920-953-2 (1-598) x US-11-056-355B-51768 (1-210)

QY 530 GGGCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGATGAGCGC 471  
Db 13 GlyArgGlyGlyGlnAlaArgSerGluGlnProThrLeuArgArgTrpProArg 32  
QY 470 -----TCAGGCTGGGTGG--GTTAATGAAATCAGTTGGGTGGCACTTG 426  
Db 33 ArgAlaArgSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 52  
QY 425 TTGGGNAAG----- 417  
Db 53 ArgGlySerAlaSerAlaArgArgProArgArgArgProArgArgProArgPro 72  
QY 416 -----TCAATTCGTGGGGTGGACTCCACCCTCGCGGGCGTGC 375  
Db 73 ProThrGlyArgCysGlySerProAlaArgArgProSerThrSerThrGlyArgSer 92  
QY 374 TGGATCATCTCTGTGAGCCCATCTCTTGACGCTCTCTCAAGGTACTGCTTGATC 315  
Db 93 SerAlaThrThrAlaSerThrPro--SerAlaLeuGlySerProArgSerThrCysSer 111  
QY 314 TTGTCAAGTGGCGGTGGTCCAGCCGTGGCCCTTGACCATGGCGGTGCGTCTGATC 255  
Db 112 ThrThrTrpThrProTrpThrArgThrTrpProArgThr--TrpArgAlaArgSer--- 129  
QY 254 ATGCTTCGGCCCTTGATGCTGCTCGG-----CCAAACAGCAAGCTCATG 207  
Db 130 -----SerAlaProGlySerArgThrProThrSerSerProPro 142  
QY 206 AACTTGACCTGCTCATCTCTGCTCTTGATGTCAGGACTCGAAGAGGGCAGCAGC 147  
Db 143 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 157  
QY 146 TCGGGTTCAGCAGCACCTTATCTAGAGGTGTCACCGCCAGCTTCATGCTCTCTGCG 87  
Db 158 SerAlaSerSerThrValAla-GlyProCysSerProProSerAla----- 173  
QY 86 CCGCCAGGTATCAAAAGCTTCTTGGCCCGCATCCCGCTTCGCGTCTCTGCTG 27  
Db 174 ----ProSerProSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 192  
QY 26 CTGGTGG 20  
Db 192 rtrpTrp 194

## RESULT 6

US-10-953-349-28428  
; Sequence 28428, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 28428  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (306)..(306)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-953-349-28428

## Alignment Scores:

Pred. No.: 0.000939 Length: 358  
Score: 123.50 Matches: 62  
Percent Similarity: 33.5% Conservative: 9  
Best Local Similarity: 29.2% Mismatches: 62  
Query Match: 11.0% Indels: 79  
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-10-953-349-28428 (1-358)

QY 21 CACGACGACACACAGAGACGCGGAGCGGATCGCGGCGCAAGAGCTGTTGTATGACCT 80  
Db 41 HisSerHisAspArg-----Ala 46  
QY 81 GGGCGCGGAGAGGATGAAGCTGCGGTTGACAC----- 116  
Db 47 GlyArgArgArgProHisSerIleProArgArgHisAspAlaValArgLeuGlnArgArg 66  
QY 117 CTTTACGATAGGTCTGCTGCTGACCGGAGCTGCTGCTTCTTCGAGTCCCTGGACAT 176  
Db 67 ProIleArgArgGlyAlaGly-----ArgArgValProIlePro 79  
QY 177 GCAAGAGCAGAGATCAAGCAGCTCAAGTTCAATGAGCTGCTGTTGGCGGAGCAGA--- 233  
Db 80 ArgArgProGluAlaProAlaGlyGluValArgAlaGlyArgAlaProArgProArgArg 99  
QY 234 -----CCAATACAGGCGCGCAAGCAT----- 254  
Db 100 ValArgGlnGlyLeuProGlyGlnGlyHisProHisGlyProGlyArgGlyHisGlnVal 119  
QY 255 -----GTACACGCGACA 266  
Db 120 ValProGlnProAlaGlyArgArgAlaArgGlyGlyGlyLeuArgArgValArgArgHis 139  
QY 267 CGCCCATCTGTTCAAGGCGCGCTGACCCACCGCCACTTTTGACAGATCAAGCAGTA 326  
Db 140 ArgAlaGlyGlyHisProGlnProProAlaProPro----- 152  
QY 327 CTTTGAGAGAGCGCTCAAGAGATGGCGTCAAGCAGGA-----TGTGATCCA 374  
Db 153 ProArgArgGluAlaProArgAspSerArgHisAlaGlnGluGlyProLeuCysProArg 172  
QY 375 GCACGCGCGGAGTGGTGGAGTCCACCGCGGACGAATTTGACTTCCCAACACTGCGCG 434  
Db 173 ProArgArgArg-----ArgArgAlaValLeuAlaArgArgLeuArg 186  
QY 435 ACCCACTGATTTTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGAGC 494  
Db 187 ArgPro-----HisAspGlyGlyProArgAlaAlaLeuLeuProThrAlaArgVal 203  
QY 495 GGGGAGCGCGAGTTGCGGAGCGCGCGCCAGGGGCGCC 530  
Db 204 GlyArgProValLeuProLeuProArgArgLeuPro 215

## RESULT 7

US-11-056-355B-3621  
; Sequence 3621, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT FILING DATE: 2005-02-14  
PRIORITY APPLICATION NUMBER: 60/544,190  
PRIORITY FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 3621  
LENGTH: 375  
TYPE: prt  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)..(375)  
OTHER INFORMATION: Ceres Seq. ID no. 12414168  
US-11-056-355B-3621

Alignment Scores:  
Pred. No.: 0.00208 Length: 375  
Score: 120.00 Matches: 56  
Percent Similarity: 37.2% Conservativity: 21  
Best Local Similarity: 27.1% Mismatches: 92  
Query Match: 10.7% Indels: 38  
DB: 7 Gaps: 8

US-09-920-953-2 (1-598) x US-11-056-355B-3621 (1-375)

QY 5 TGCCTGCAGACGGCGCCAGCAGACAGACGGCGGATCGGGCGCAAGA 64  
DB 172 CysArgAlaThrArgProAlaAlaProSerArgThrThrSerProCysAla----- 188

QY 65 ACCTGTTTGATGACCTGGCGCGCGAGAGGATGAAGCTGGCGGTGCACCTTCTAGC 124  
DB 189 -----SerValAlaArgProArgThrTrpProProSerPro----- 200

QY 125 ATAAGGTGCTGCTGACCGCGAGCTGCTCCCTTCTTCGAGTCCCTGGACATGCAAGAGC 184  
DB 201 -----CysGlyAspThrSerSerCysHisSerSerAlaAlaThrArgAlaArgGly 218

QY 185 AGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTGTTGGCGGAGCAGACCAATACAAG 244  
DB 219 ArgArgProSerAlaProThrLeuSerSerThrGlyProSerThrThrAlaThrGly 238

QY 245 GCCGAAGCATGTACGACGACACAGCCATCTGCTCAAGGCCCGCGCTGGACACCGCC 304  
DB 239 AlaCysArgCys-----ArgArgAlaProArgProThrThrPro 251

QY 305 ACTTTGACAAGATCAAGCAGTACCTTGGAGACGCTGCAAGAGATGGCGTCAAGCAGG 364  
DB 252 TrpProThrArgSerAlaProAlaArg-----ArgArgTrpThrProSer--- 266

QY 365 ATGTGATCAGACGCGCGGAGTGGTGGAGTCCACCGCG-----ACGAATTG 415  
DB 267 -----SerSerArgProPro-----TrpSerSerAlaAlaThrSerSerThr 282

QY 416 ACTTNCACCAACTCGCCACCACTGATTTCATTAAACCCACCCAGCTGAGCGCT 475  
DB 283 ThrAlaProSerThrThrProGlySerGlyProGlyProGlySerProSerTrpSerGly 302

QY 476 CATTCATCGATTGAGCGGGAGCG-----CCAGTTCGCCAGCGC 517  
DB 303 ThrSerThrAlaSerSerThrAlaSerProSerThrProGlyProThrProPro 322

QY 518 GCCCAGGGGCCAGGAGCTCAATCGTTTGGCAGCCCTGCTGCATTGAAGAGCCAT 577  
DB 323 SerSerCysAlaSerSerSerAlaSerSerThrProThrAlaAlaSerThrSerThrAsp 342

QY 578 CAGCCATTTCGACCAACG 598  
DB 343 ThrSerValSerAsnSerSer 349

## RESULT 8

US-11-056-355B-3480  
Sequence 3480, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT FILING DATE: 2005-02-14  
PRIORITY APPLICATION NUMBER: 60/544,190  
PRIORITY FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 3480  
LENGTH: 309  
TYPE: prt  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)..(309)  
OTHER INFORMATION: Ceres Seq. ID no. 12367975  
US-11-056-355B-3480

Alignment Scores:  
Pred. No.: 0.00348 Length: 309  
Score: 117.50 Matches: 75  
Percent Similarity: 36.7% Conservativity: 15  
Best Local Similarity: 30.6% Mismatches: 86  
Query Match: 10.5% Indels: 69  
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-056-355B-3480 (1-309)

QY 15 CGCGCCACCAACGAC-----CACAGACGCGCGGAGCGGATCGGGCGCAAGAAGCT 68  
DB 57 ArgGlyHisArgHisProSerHisArgProLeuAlaSerValArgGln----- 72

QY 69 GTTTGATGACCTGGCGCGCGAGGAGGATGAAGCTGCG----- 107  
DB 73 -----ArgArgArgArgGlyArgAlaGlyArgGlyGlyArgGlyGlu 87

QY 108 ---GTTTACACCTCTACGA-----TAAGTGCT 134  
DB 88 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspHisGlyAla 107

QY 135 GGCTGACCGCGAGCTGCTGCTTCAGTCCCTGGACATGCA-----AGAGCA 185  
DB 108 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 127

QY 186 GAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTGGCGGAGCAGACCA----- 236  
DB 128 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 147

QY 237 ATACAGGCGCGAGCATGTACGACGACAGCCCATCTGTCAGGCGCGCGCTGGA 296  
DB 148 LeuGluGlyGlyValArgProArgAlaAlaAlaAlaAlaGlyCysArgGlyArg 167

QY 297 CCACCGCCACTTTCACAGATCAACAGCTACT-----TGGAGAGACGCT 341  
DB 168 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeuGlnArgGlyAla 187

QY 342 GCA-----AGAGATGGCGGT-----CAAGCAGGATGTGATCCAGCA 377  
DB 188 GlyGlyValArgGlnSerAspGlyArgAlaGlyValGlnAlaAlaGlyAlaAsp--ArgS 207

QY 378 CGCGCGCGAGTGTGGAGTCCACCGCGAGCAAT---TTGACTTNCACCAACTGGCG 434  
DB 207 erGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProAspAspLeuH 227

QY 435 ACCCAACTGATTTTCATTAAACCCACCCAGCGCTCATTCATCGATTTTGAGC 494



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; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40564
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-40564

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Alignment Scores:	
Pred. No.:	0.00612
Score:	115.00
Percent Similarity:	36.6%
Best Local Similarity:	29.3%
Query Match:	10.2%
DB:	6
Length:	317
Matches:	48
Conservative:	12
Mismatches:	74
Indels:	30
Gaps:	7

US-09-920-953-2 (1-598) x US-10-449-902-40564 (1-317)

439	QY	TGGGTGCGCAGTGTGTGGNAAGTCAAATT	CGTCGCGGGTGAATCCACCACCTCCGCGCG	380
129	Db	TrpIleLysSerSerPheVal	-----TrpPheCysSerAlaIleArg	143
		:::		
379	QY	CGTCTGGATCACATCTCTGCTTGAAGCCCAATCT	TGTCAGCGCTCTCTCAAAGT-----	326
144	Db	ArgThrTrpCysAlaProAlaAlaAlaAlaThr	ThrAlaSerSerAlaAlaAlaProPro	163
325	QY	-----ACTGTTTGATCTTGTCAAAGTGGCGGT	TCCAGCGCGTGGCCCTTCACCA	275
164	Db	ArgThrProThrAlaProSerTyrThrProSer	SerAlaProProArgTrpArgAlaPro	183
274	QY	GATGGCGGTGTGCGTCGTACATGCTTCGGC-	-----CCTTGATTTGGTCTG	230
184	Db	ThrArgArgThrAlaAlaThrAlaThrSerCys	ThrAlaArgProProSerThrSerAla	203
229	QY	CTCGCCAAACACGAAGCTCATGAACCTTGACCT	TTCATCTTCTCTCTTGTCATGTCCTCA	170
204	Db	ArgAlaArgAlaArgProAla-----	ProAlaArgThrProAlaAlaAlaSerAla	220
169	QY	GGGACTCGAAGAGGGCAGCAGCT-----	CCGGGTGAGCCACACACTTATCGTAGA	119
221	Db	AlaArgArgArgSerSerAlaThrSerProPro	ThrThrProGlyProSerArgArg	240
118	QY	-----AGGTCTCAACCGCCAGCTTCATGCT	TGCGCTTGGCGCGCCACAGGTAT	74
241	Db	SerAlaThrArgSerArgAlaGlySerProCys	ArgCys-----ProGlyGly	256
73	QY	CAACACGCTCTTGGCGCCCGCATCCCGCT	TCTCCCGCTCTCTGTGGTCTGGTGGCCGCGT	14
257	Db	AlaThrSerSerGlyArgThrThrAlaProCys	SerTyrTrpCysProArgProArg	276
13	QY	CTGCAGCGACGC	2	
277	Db	AlaAlaSerAla	280	

RESULT 13

RESULT 13  
US-11-056-355B-16356  
; Sequence 16356, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav

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; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 16356
; LENGTH: 352
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(352)
; OTHER INFORMATION: Ceres Seq. ID no. 12405305
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (256)..(256)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-056-355B-16356

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Alignment Scores:	
Pred. No.:	0.011
Score:	112.50
Percent Similarity:	32.5%
Best Local Similarity:	28.6%
Query Match:	10.0%
DB:	7
Gaps:	13
Indels:	8
Mismatches:	56
Conservative:	8
Matches:	59
Length:	352

US-09-920-953-2 (1-598) x US-11-056-355B-16356 (1-352)

555	QY	GTGGGCAAAACGATTGCGGC-----TCCTGGGCCCTCGGGCGCGCTCGGCACAACTGGC	500
124	Db	AlaGlySerArgGlyThrGlyArgProSerTrpSerProArgThrArgSerTrpThrGly	143
501	QY	-----GCTCCCGCGCTCA-----AAA	487
144	Db	ProThrCysPheSerCysProArgSerArgProSerThrGlyProAlaSerCysArg	163
486	QY	TCGATGGAATGAGCGCTCAGCGCTGGGTTTCGGTTTAATGAAATCAGTTGGGTGGCGAGTT	427
164	Db	ArgAlaArgProArgSerGlyThrArgTrp-----	173
426	QY	GTGGGNAAGTCAAAATTCGTGGCGGTGAGACTCACCACTCCGCGCGGTCTCGATCAC	367
174	Db	-----ArgAlaThrLeuProArgCys---SerAlaTrpProAlaCysTrp-----	188
366	QY	ATCCTGTTGACGCCCATCTCTTGCAGCGCTCTCCAAAGTACTGCTTGATCTGTCAAA	307
188	Db	-----	188
306	QY	GTGGCGGTGTCGAGCGCTGGCGCTTGACAGATGGCGGTGTCGTCGTACATCTTCG	247
189	Db	-----ArgProTrpProArgThr---TrpAlaTrpArgThr-----	199
246	QY	GCCCTTGATTGTCCTCGCCGCAACAGAGCTCATGAACTTGACCTGCTTCATCTT	187
200	Db	---ProArgGlyTrpProGlySerPro---ThrArgArg-----ProcysAlaSerT	215
186	QY	CTGCTCTTCATGTCACGGAGCTCGAAGA---AGGGCAGCAGCTCCGGGTACGCCAGCAC	130
215	Db	---hrThr-----ThrArgArgAlaArgThrAlaGlyAlaGlyCysTrpAlaC	230
129	QY	CTTATCGTAGAAGGTGTCAACCGCCAGCTTCATGCTCTCTGCGC-----	86
230	Db	ysArgArgThrArgThrProProAlaSerArgCysCysSerArgSerAlaProSerArg	250
85	QY	-----CGCCCGGTCATCAACAGCTCTTGTGGCCCGCATCCCGTTCGCCGCTCTCTGT	31
250	Db	lyCysArgSerGlyGly****AlaArgGlySerAlaSerThrProSerProGluArg----	268

QY 30 GGTGCTGGTGGCCG 17  
Db 269 -----TTPTrpPro 271

## RESULT 14

US-11-056-355B-16355  
; Sequence 16355, Application US/11056355B  
; Publication No. US20060150283A1

## GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056,355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544,190

; PRIOR FILING DATE: 2004-02-13

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 16355

; LENGTH: 355

; TYPE: prt

; ORGANISM: Zea mays subsp. mays

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(355)

; OTHER INFORMATION: Ceres Seq. ID no. 12405304

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (259)..(259)

; OTHER INFORMATION: Xaa is any aa, unknown or other

US-11-056-355B-16355

Alignment Scores:  
Pred. No.: 0.011 Length: 355  
Score: 112.50 Matches: 59  
Percent Similarity: 32.5% Conservative: 8  
Best Local Similarity: 28.6% Mismatches: 56  
Query Match: 10.0% Indels: 83  
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-056-355B-16355 (1-355)

QY 555 GCTGGCAACGATTGCGCC-----TCCTGGGCCCCCTGGGCGCGCTGGCACTGGC 502

Db 127 AlAGlySerArgGlyThrGlyArgProSerTrpSerProArgThrArgSerTrpThrGly 146

QY 501 -----GCTCCCGCTCA-----AAA 487

Db 147 ProThrCysPheSerCysProArgSerArgProSerThrGlyProArgAlaSerCysArg 166

QY 486 TCGATGGAATGAGCGCTCAGGCTGGGTTGGGTTAATGAAATCAGTTGGGTGCGCAGTT 427

Db 167 \*ArgAlaArgProArgSerGlyThrArgTrp----- 176

QY 426 GTTGGGNAAGTCAAAATCGTCGCGGGTGAGTCCACACTCGGCGGCGTGTGATCAAC 367

Db 177 -----ArgAlaThrLeuProArgCys---SerAlaTrpProProAlaCysTrp----- 191

QY 366 ATCTGCTTGACGCCCATCTCTTGACGCGTCTCTCAAGGACTCTGCTGATCTTGTCAAA 307

Db 191 ----- 191

QY 306 GTGGCGGTGGTCCAGCGCTGGCCCTTGACACAGATGGCGTGTGGTGTGATCATCTTCG 247

Db 192 -----ArgProTrpProArgThr---TrpAlaTrpArgThr----- 202

QY 246 GCCCTGTATTGTCGTCTCGCCCAACACAGAGCTCATGAACTTGACCTGCTTCATCTT 187

Db 203 -ProArgGlyTrpProGlySerPro-ThrArgArg-----ProCysAlaSerT 218

QY 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

Db 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

QY 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

Db 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

QY 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

Db 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

QY 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

Db 186 CTGCTCTTGATGTCACGAGGACTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGCAC 130

Db 218 hrThr-----ThrArgAlaAlaArgThrAlaGlyAlaGlyCysTrpAlaC 233

QY 129 CTTATCGTAGAAGGTGTCAACCGCAGCTTCATCGCTTCTGCGC----- 86

Db 233 ysArgArgThrArgThrProProAlaSerArgCysCysSerArgSerAlaProSerArgG 253

QY 85 -----CGCCGAGGTATCAACACAGCTTCTTGGCGCCGCGCATCCGCTTCCGCGCTCTCTGT 31

Db 253 lyCysArgSerGlyGly\*\*\*AlaArgGlySerAlaSerThrProSerProGluArg----- 271

QY 30 GGTGCTGGTGGCCG 17

Db 272 -----TTPTrpPro 274

## RESULT 15

US-10-953-349-33290

; Sequence 33290, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 33290

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-33290

Alignment Scores:  
Pred. No.: 0.0108 Length: 199  
Score: 112.00 Matches: 58  
Percent Similarity: 34.1% Conservative: 14  
Best Local Similarity: 27.5% Mismatches: 78  
Query Match: 10.0% Indels: 61  
DB: 6 Gaps: 11

US-09-920-953-2 (1-598) x US-10-953-349-33290 (1-199)

QY 536 GCTCTGGGCGCCCT-----GGGCGCGCTCGGAACCTGGCGCTCCCGCTCAAAAT 486

Db 8 SerProLeuProProLeuLeuSerSerArgProThrHisLeuLeuAlaProAlaProGly 27

QY 485 CGATGGAATGAGCGCTCAGGC-----TGGGGT 459

Db 28 LysTrpArgProArgCysGlyArgCysCysTrpTrpTrpProCysArgArgTrpArg 47

QY 458 TGGTTAATGAAATCAGTTGGGTGCGC----- 431

Db 48 TrpProArg-ThrAlaProTrpArgArgArgProArgArgArgArgArgArgTrpAr 67

QY 430 -----AGTTCTGGGNAAGTCAAAATTCGTGCG-----GG 402

Db 67 gCysSerAlaAlaThrSerCysArgGlyAlaCysCysArgArgGlySerArgArgSerGl 87

QY 401 GTGACATCCACCACTCCGGCGG---CGTGCTGGA---TCACATCCTGCTTGACGCCCATC 348

Db 87 yThrThrProProArgGluArgSerArgProGlyTrpTrpArgProAlaArgAlaSe 107

QY 347 TCTTTCAGCGCTCTCTCCAAAGGTACTGCTTGTATCTTGTCAAAAGTGGCGGTGGTCCAGGCCG 288

Db 107 xArgSerAlaSer-----AlaThrThrProProSerProGlySerSerAlaProAlaAr 125

QY 287 TGGCCCTTGACCAAGATGGCGGTGCGTCGTACA-----TGCTTCGCGCCCTTGATTGG 234

Db 125 gSerProThrSerProAlaSerProArgTrpSerSerCysGlySerProSer----- 143

QY 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

Db 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

QY 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

Db 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

QY 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

Db 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

QY 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

Db 233 TCTGCTCGCCAAACACGAGCTCATGACCTTGACCTTCATCTTCTGCTCTTCGTCATG 174

```

Db      144 -----ThrThrSerArgSerThrSerProProAlaSerSerThrThrSerAl 161
Qy      173 TCCAGGGACTCGAAGAGGCGAGCTCCGGGTCCAGCCAGCACCTTATCGTAGAAGGTG 114
Db      161 a---SerSerArgSerThrSerArgSerPro----- 170
Qy      113 TCAACCGCCAGCTTCATGCCTTCTCGCGCGCCAGGTCATCAAAACAGCTTCTTGGCCCG 54
Db      171 -----SerSerThrArgArgProAlaArgProThrArgSerCysArgSe 186
Qy      53 CATCCCGCTTCGCCGCTCTCTGTGTGTGGTGG 23
Db      186 rPheLeuIleLeuAlaSerLeuSerArgTrp 196

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Search completed: August 11, 2006, 10:35:56  
 Job time : 23 secs